

10/077130
07-30-04

BC

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
25 April 2002 (25.04.2002)

PCT

(10) International Publication Number
WO 02/33099 A2

(51) International Patent Classification⁷: C12N 15/54,
9/12, A01K 67/027, C07K 16/40, C12Q 1/68, 1/48, G01N
33/50, A61K 38/45

(21) International Application Number: PCT/US01/47728

(22) International Filing Date: 20 October 2001 (20.10.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/242,410 20 October 2000 (20.10.2000) US
60/244,068 27 October 2000 (27.10.2000) US
60/245,708 3 November 2000 (03.11.2000) US
60/247,672 9 November 2000 (09.11.2000) US
60/249,565 16 November 2000 (16.11.2000) US
60/252,730 22 November 2000 (22.11.2000) US
60/250,807 1 December 2000 (01.12.2000) US

(71) Applicant (for all designated States except US): INCYTE GENOMICS, INC. [US/US]; 3160 Porter Drive, Palo Alto, CA 94304 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): GURURAJAN, Rajagopal [US/US]; 5591 Dent Avenue, San Jose, CA 95118 (US). BAUGHN, Mariah, R. [US/US]; 14244 Santiago Road, San Leandro, CA 94577 (US). WALIA, Narinder, K. [US/US]; 890 David Street, #205, San Leandro, CA 94577 (US). ELLIOTT, Vicki, S. [US/US]; 3770 Polton Place Way, San Jose, CA 95121 (US). XU, Yuming [US/US]; 1739 Walnut Drive, Mountain View, CA 94040 (US). ARVIZU, Chandra [US/US]; 490 Sherwood Way #1, Menlo Park, CA 94025 (US). YAO, Monique, G. [US/US]; 1189 Woodgate Drive, Carmel, IN 46033 (US). RAMKUMAR, Jaya [IN/US]; 34359 Maybird Circle, Fremont, CA 94555 (US). DING, Li [CN/US]; 3353 Alma Street #146, Palo Alto, CA 94306 (US). TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). HAFALIA, April, J., A. [US/US]; 2227 Calle de Primavera, Santa Clara, CA 95054 (US). NGUYEN, Danniel, B. [US/US]; 1403 Ridgewood Drive, San Jose, CA 95118 (US). GANDHI, Ameena, R. [US/US]; 705 5th Avenue, San Francisco, CA 94118 (US). LU, Yan [CN/US]; 3885 Corrnia Way, Palo Alto, CA 94303 (US). YUE,

Henry [US/US]; 826 Lois Avenue, Sunnyvale, CA 94087 (US). BURFORD, Neil [GB/US]; 105 Wildwood Circle, Durham, CT 06422 (US). BANDMAN, Olga [US/US]; 366 Anna Avenue, Moutain View, CA 94043 (US). TRIBOULEY, Catherine, M. [FR/US]; 1121 Tennessee, #5, San Francisco, CA 94107 (US). LAL, Preeti, G. [IN/US]; P.O. Box 5142, Santa Clara, CA 95056 (US). RECIPON, Shirley, A. [US/US]; 85 Fortuna Avenue, San Francisco, CA 94115 (US). LU, Dyung, Aina, M. [US/US]; 233 Coy Drive, San Jose, CA 95123 (US). BOROWSKY, Mark, L. [US/US]; 122 Orchard Avenue, Redwood City, CA 94061 (US). THORNTON, Michael [US/US]; 9 Medway Road, Woodside, CA 94062 (US). SWARNAKER, Anita [CA/US]; 8 Locksley Avenue, #5D, San Francisco, CA 94122 (US). THANGAVELU, Kavitha [IN/US]; 1950 Montecito Avenue #23, Mountain View, CA 94304 (US). KHAN, Farrah, A. [IN/US]; 3617 Central Road, #102, Glenview, IL 60025 (US). ISON, Craig, H. [US/US]; 1242 Weathersfield Way, San Jose, CA 95118 (US).

(74) Agents: HAMLET-COX, Diana et al.; Incyte Genomics, Inc., 3174 Porter Drive, Palo Alto, CA 94304 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARJPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN KINASES

(57) Abstract: The invention provides human human kinases (PKIN) and polynucleotides which identify and encode PKIN. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of PKIN.

WO 02/33099 A2

HUMAN KINASES

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human kinases and to the
5 use of these sequences in the diagnosis, treatment, and prevention of cancer, immune disorders,
disorders affecting growth and development, cardiovascular diseases, and lipid disorders, and in the
assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid
sequences of human kinases.

10

BACKGROUND OF THE INVENTION

Kinases comprise the largest known enzyme superfamily and vary widely in their target
molecules. Kinases catalyze the transfer of high energy phosphate groups from a phosphate donor to
a phosphate acceptor. Nucleotides usually serve as the phosphate donor in these reactions, with most
kinases utilizing adenosine triphosphate (ATP). The phosphate acceptor can be any of a variety of
15 molecules, including nucleosides, nucleotides, lipids, carbohydrates, and proteins. Proteins are
phosphorylated on hydroxyamino acids. Addition of a phosphate group alters the local charge on the
acceptor molecule, causing internal conformational changes and potentially influencing intermolecular
contacts. Reversible protein phosphorylation is the primary method for regulating protein activity in
eukaryotic cells. In general, proteins are activated by phosphorylation in response to extracellular
20 signals such as hormones, neurotransmitters, and growth and differentiation factors. The activated
proteins initiate the cell's intracellular response by way of intracellular signaling pathways and second
messenger molecules such as cyclic nucleotides, calcium-calmodulin, inositol, and various mitogens,
that regulate protein phosphorylation.

Kinases are involved in all aspects of a cell's function, from basic metabolic processes, such
25 as glycolysis, to cell-cycle regulation, differentiation, and communication with the extracellular
environment through signal transduction cascades. Inappropriate phosphorylation of proteins in cells
has been linked to changes in cell cycle progression and cell differentiation. Changes in the cell cycle
have been linked to induction of apoptosis or cancer. Changes in cell differentiation have been linked
to diseases and disorders of the reproductive system, immune system, and skeletal muscle.

30 There are two classes of protein kinases. One class, protein tyrosine kinases (PTKs),
phosphorylates tyrosine residues, and the other class, protein serine/threonine kinases (STKs),
phosphorylates serine and threonine residues. Some PTKs and STKs possess structural
characteristics of both families and have dual specificity for both tyrosine and serine/threonine

residues. Almost all kinases contain a conserved 250-300 amino acid catalytic domain containing specific residues and sequence motifs characteristic of the kinase family. The protein kinase catalytic domain can be further divided into 11 subdomains. N-terminal subdomains I-IV fold into a two-lobed structure which binds and orients the ATP donor molecule, and subdomain V spans the two lobes. C-terminal subdomains VI-XI bind the protein substrate and transfer the gamma phosphate from ATP to the hydroxyl group of a tyrosine, serine, or threonine residue. Each of the 11 subdomains contains specific catalytic residues or amino acid motifs characteristic of that subdomain. For example, subdomain I contains an 8-amino acid glycine-rich ATP binding consensus motif, subdomain II contains a critical lysine residue required for maximal catalytic activity, and subdomains VI through IX comprise the highly conserved catalytic core. PTKs and STKs also contain distinct sequence motifs in subdomains VI and VIII which may confer hydroxyamino acid specificity.

In addition, kinases may also be classified by additional amino acid sequences, generally between 5 and 100 residues, which either flank or occur within the kinase domain. These additional amino acid sequences regulate kinase activity and determine substrate specificity. (Reviewed in 15 Hardie, G. and Hanks, S. (1995) The Protein Kinase Facts Book, Vol I p.p. 17-20 Academic Press, San Diego, CA.). In particular, two protein kinase signature sequences have been identified in the kinase domain, the first containing an active site lysine residue involved in ATP binding, and the second containing an aspartate residue important for catalytic activity. If a protein analyzed includes the two protein kinase signatures, the probability of that protein being a protein kinase is close to 100% 20 (PROSITE: PDOC00100, November 1995).

Protein Tyrosine Kinases

Protein tyrosine kinases (PTKs) may be classified as either transmembrane, receptor PTKs or nontransmembrane, nonreceptor PTK proteins. Transmembrane tyrosine kinases function as receptors for most growth factors. Growth factors bind to the receptor tyrosine kinase (RTK), which 25 causes the receptor to phosphorylate itself (autophosphorylation) and specific intracellular second messenger proteins. Growth factors (GF) that associate with receptor PTKs include epidermal GF, platelet-derived GF, fibroblast GF, hepatocyte GF, insulin and insulin-like GFs, nerve GF, vascular endothelial GF, and macrophage colony stimulating factor.

Nontransmembrane, nonreceptor PTKs lack transmembrane regions and, instead, form 30 signaling complexes with the cytosolic domains of plasma membrane receptors. Receptors that function through non-receptor PTKs include those for cytokines and hormones (growth hormone and prolactin), and antigen-specific receptors on T and B lymphocytes.

Many PTKs were first identified as oncogene products in cancer cells in which PTK

activation was no longer subject to normal cellular controls. In fact, about one third of the known oncogenes encode PTKs. Furthermore, cellular transformation (oncogenesis) is often accompanied by increased tyrosine phosphorylation activity (Charbonneau, H. and Tonks, N. K. (1992) *Annu. Rev. Cell Biol.* 8:463-93). Regulation of PTK activity may therefore be an important strategy in controlling some types of cancer.

Protein Serine/Threonine Kinases

Protein serine/threonine kinases (STKs) are nontransmembrane proteins. A subclass of STKs are known as ERKs (extracellular signal regulated kinases) or MAPs (mitogen-activated protein kinases) and are activated after cell stimulation by a variety of hormones and growth factors. 10 Cell stimulation induces a signaling cascade leading to phosphorylation of MEK (MAP/ERK kinase) which, in turn, activates ERK via serine and threonine phosphorylation. A varied number of proteins represent the downstream effectors for the active ERK and implicate it in the control of cell proliferation and differentiation, as well as regulation of the cytoskeleton. Activation of ERK is normally transient, and cells possess dual specificity phosphatases that are responsible for its down- 15 regulation. Also, numerous studies have shown that elevated ERK activity is associated with some cancers. Other STKs include the second messenger dependent protein kinases such as the cyclic-AMP dependent protein kinases (PKA), calcium-calmodulin (CaM) dependent protein kinases, and the mitogen-activated protein kinases (MAP); the cyclin-dependent protein kinases; checkpoint and cell cycle kinases; proliferation-related kinases; 5'-AMP-activated protein kinases; and kinases 20 involved in apoptosis.

The second messenger dependent protein kinases primarily mediate the effects of second messengers such as cyclic AMP (cAMP), cyclic GMP, inositol triphosphate, phosphatidylinositol, 3,4,5-triphosphate, cyclic ADPribose, arachidonic acid, diacylglycerol and calcium-calmodulin. The PKAs are involved in mediating hormone-induced cellular responses and are activated by cAMP 25 produced within the cell in response to hormone stimulation. cAMP is an intracellular mediator of hormone action in all animal cells that have been studied. Hormone-induced cellular responses include thyroid hormone secretion, cortisol secretion, progesterone secretion, glycogen breakdown, bone resorption, and regulation of heart rate and force of heart muscle contraction. PKA is found in all animal cells and is thought to account for the effects of cAMP in most of these cells. Altered PKA 30 expression is implicated in a variety of disorders and diseases including cancer, thyroid disorders, diabetes, atherosclerosis, and cardiovascular disease (Isselbacher, K.J. et al. (1994) Harrison's Principles of Internal Medicine, McGraw-Hill, New York, NY, pp. 416-431, 1887).

The casein kinase I (CKI) gene family is another subfamily of serine/threonine protein

kinases. This continuously expanding group of kinases have been implicated in the regulation of numerous cytoplasmic and nuclear processes, including cell metabolism, and DNA replication and repair. CKI enzymes are present in the membranes, nucleus, cytoplasm and cytoskeleton of eukaryotic cells, and on the mitotic spindles of mammalian cells (Fish, K.J. et al., (1995) J. Biol. Chem. 5 270:14875-14883.

The CKI family members all have a short amino-terminal domain of 9-76 amino acids, a highly conserved kinase domain of 284 amino acids, and a variable carboxyl-terminal domain that ranges from 24 to over 200 amino acids in length (Cegielska, A. et al., (1998) J. Biol. Chem. 273:1357-1364.) The CKI family is comprised of highly related proteins, as seen by the identification of isoforms of casein kinase I from a variety of sources. There are at least five mammalian isoforms, α , β , γ , δ , and ϵ . Fish et al., identified CKI-epsilon from a human placenta cDNA library. It is a basic protein of 416 amino acids and is closest to CKI-delta. Through recombinant expression, it was determined to phosphorylate known CKI substrates and was inhibited by the CKI-specific inhibitor CKI-7. The human gene for CKI-epsilon was able to rescue yeast with a slow-growth phenotype caused by 10 deletion of the yeast CKI locus, HRR250 (Fish et al, *supra*.)

The mammalian circadian mutation tau was found to be a semidominant autosomal allele of CKI-epsilon that markedly shortens period length of circadian rhythms in Syrian hamsters. The tau locus is encoded by casein kinase I-epsilon, which is also a homolog of the Drosophila circadian gene double-time. Studies of both the wildtype and tau mutant CKI-epsilon enzyme indicated that the 20 mutant enzyme has a noticeable reduction in the maximum velocity and autophosphorylation state. Further, *in vitro*, CKI-epsilon is able to interact with mammalian PERIOD proteins, while the mutant enzyme is deficient in its ability to phosphorylate PERIOD. Lowrey et al., have proposed that CKI-epsilon plays a major role in delaying the negative feedback signal within the transcription-translation-based autoregulatory loop that composes the core of the circadian mechanism. Therefore the CKI-epsilon enzyme is an ideal target for pharmaceutical compounds influencing circadian rhythms, jet-lag 25 and sleep, in addition to other physiologic and metabolic processes under circadian regulation (Lowrey, P.L. et al., (2000) Science 288:483-491.)

Calcium-Calmodulin Dependent Protein Kinases

Calcium-calmodulin dependent (CaM) kinases are involved in regulation of smooth muscle contraction, glycogen breakdown (phosphorylase kinase), and neurotransmission (CaM kinase I and CaM kinase II). CaM dependent protein kinases are activated by calmodulin, an intracellular calcium receptor, in response to the concentration of free calcium in the cell. Many CaM kinases are also activated by phosphorylation. Some CaM kinases are also activated by autophosphorylation or by 30

other regulatory kinases. CaM kinase I phosphorylates a variety of substrates including the neurotransmitter-related proteins synapsin I and II, the gene transcription regulator, CREB, and the cystic fibrosis conductance regulator protein, CFTR (Haribabu, B. et al. (1995) EMBO Journal 14:3679-3686). CaM kinase II also phosphorylates synapsin at different sites and controls the synthesis of catecholamines in the brain through phosphorylation and activation of tyrosine hydroxylase. CaM kinase II controls the synthesis of catecholamines and serotonin, through phosphorylation/activation of tyrosine hydroxylase and tryptophan hydroxylase, respectively (Fujisawa, H. (1990) BioEssays 12:27-29). The mRNA encoding a calmodulin-binding protein kinase-like protein was found to be enriched in mammalian forebrain. This protein is associated with vesicles in both axons and dendrites and accumulates largely postnatally. The amino acid sequence of this protein is similar to CaM-dependent STKs, and the protein binds calmodulin in the presence of calcium (Godbout, M. et al. (1994) J. Neurosci. 14:1-13).

Mitogen-Activated Protein Kinases

The mitogen-activated protein kinases (MAP) which mediate signal transduction from the cell surface to the nucleus via phosphorylation cascades are another STK family that regulates intracellular signaling pathways. Several subgroups have been identified, and each manifests different substrate specificities and responds to distinct extracellular stimuli (Egan, S.E. and Weinberg, R.A. (1993) Nature 365:781-783). MAP kinase signaling pathways are present in mammalian cells as well as in yeast. The extracellular stimuli which activate MAP kinase pathways include epidermal growth factor (EGF), ultraviolet light, hyperosmolar medium, heat shock, endotoxic lipopolysaccharide (LPS), and pro-inflammatory cytokines such as tumor necrosis factor (TNF) and interleukin-1 (IL-1). Altered MAP kinase expression is implicated in a variety of disease conditions including cancer, inflammation, immune disorders, and disorders affecting growth and development.

Cyclin-Dependent Protein Kinases

The cyclin-dependent protein kinases (CDKs) are STKs that control the progression of cells through the cell cycle. The entry and exit of a cell from mitosis are regulated by the synthesis and destruction of a family of activating proteins called cyclins. Cyclins are small regulatory proteins that bind to and activate CDKs, which then phosphorylate and activate selected proteins involved in the mitotic process. CDKs are unique in that they require multiple inputs to become activated. In addition to cyclin binding, CDK activation requires the phosphorylation of a specific threonine residue and the dephosphorylation of a specific tyrosine residue on the CDK.

Another family of STKs associated with the cell cycle are the NIMA (never in mitosis)-related kinases (Neks). Both CDKs and Neks are involved in duplication, maturation, and separation

of the microtubule organizing center, the centrosome, in animal cells (Fry, A.M., et al. (1998) EMBO J. 17:470-481). The NIM-related kinases also include NIK1 histidine kinases, which function in signal transmission (Yamada-Okabe, T. et al. (1999) J. Bacteriol. 181:7243-7247).

Checkpoint and Cell Cycle Kinases

5 In the process of cell division, the order and timing of cell cycle transitions are under control of cell cycle checkpoints, which ensure that critical events such as DNA replication and chromosome segregation are carried out with precision. If DNA is damaged, e.g. by radiation, a checkpoint pathway is activated that arrests the cell cycle to provide time for repair. If the damage is extensive, apoptosis is induced. In the absence of such checkpoints, the damaged DNA is inherited by aberrant 10 cells which may cause proliferative disorders such as cancer. Protein kinases play an important role in this process. For example, a specific kinase, checkpoint kinase 1 (Chk1), has been identified in yeast and mammals, and is activated by DNA damage in yeast. Activation of Chk1 leads to the arrest of the cell at the G2/M transition. (Sanchez, Y. et al. (1997) Science 277:1497-1501.) Specifically, 15 Chk1 phosphorylates the cell division cycle phosphatase CDC25, inhibiting its normal function which is to dephosphorylate and activate the cyclin-dependent kinase Cdc2. Cdc2 activation controls the entry of cells into mitosis. (Peng, C-Y et al. (1997) Science 277:1501- 1505.) Thus, activation of Chk1 prevents the damaged cell from entering mitosis. A similar deficiency in a checkpoint kinase, such as Chk1, may also contribute to cancer by failure to arrest cells with damaged DNA at other checkpoints such as G2/M.

20 Proliferation-Related Kinases

Proliferation-related kinase is a serum/cytokine inducible STK that is involved in regulation of the cell cycle and cell proliferation in human megakaryocytic cells (Li, B. et al. (1996) J. Biol. Chem. 271:19402-8). Proliferation-related kinase is related to the polo (derived from *Drosophila* polo gene) 25 family of STKs implicated in cell division. Proliferation-related kinase is downregulated in lung tumor tissue and may be a proto-oncogene whose deregulated expression in normal tissue leads to oncogenic transformation.

The RET (rearranged during transfection) proto-oncogene encodes a tyrosine kinase receptor involved in both multiple endocrine neoplasia type 2, an inherited cancer syndrome, and Hirschsprung disease, a developmental defect of enteric neurons. RET and its functional ligand, glial cell line-derived neurotrophic factor, play key roles in the development of the human enteric nervous system 30 (Pachnis, V. et al. (1998) Am. J. Physiol. 275:G183-G186).

5'-AMP-activated protein kinase

A ligand-activated STK protein kinase is 5'-AMP-activated protein kinase (AMPK) (Gao, G.

et al. (1996) J. Biol Chem. 271:8675-8681). Mammalian AMPK is a regulator of fatty acid and sterol synthesis through phosphorylation of the enzymes acetyl-CoA carboxylase and hydroxymethylglutaryl-CoA reductase and mediates responses of these pathways to cellular stresses such as heat shock and depletion of glucose and ATP. AMPK is a heterotrimeric complex comprised 5 of a catalytic alpha subunit and two non-catalytic beta and gamma subunits that are believed to regulate the activity of the alpha subunit. Subunits of AMPK have a much wider distribution in non-lipogenic tissues such as brain, heart, spleen, and lung than expected. This distribution suggests that its role may extend beyond regulation of lipid metabolism alone.

Kinases in Apoptosis

10 Apoptosis is a highly regulated signaling pathway leading to cell death that plays a crucial role in tissue development and homeostasis. Deregulation of this process is associated with the pathogenesis of a number of diseases including autoimmune disease, neurodegenerative disorders, and cancer. Various STKs play key roles in this process. ZIP kinase is an STK containing a C-terminal leucine zipper domain in addition to its N-terminal protein kinase domain. This C-terminal domain 15 appears to mediate homodimerization and activation of the kinase as well as interactions with transcription factors such as activating transcription factor, ATF4, a member of the cyclic-AMP responsive element binding protein (ATF/CREB) family of transcriptional factors (Sanjo, H. et al. (1998) J. Biol. Chem., 273:29066-29071). DRAK1 and DRAK2 are STKs that share homology with the death-associated protein kinases (DAP kinases), known to function in interferon- γ induced 20 apoptosis (Sanjo et al. supra). Like ZIP kinase, DAP kinases contain a C-terminal protein-protein interaction domain, in the form of ankyrin repeats, in addition to the N-terminal kinase domain. ZIP, DAP, and DRAK kinases induce morphological changes associated with apoptosis when transfected into NIH3T3 cells (Sanjo et al. supra). However, deletion of either the N-terminal kinase catalytic domain or the C-terminal domain of these proteins abolishes apoptosis activity, indicating that in 25 addition to the kinase activity, activity in the C-terminal domain is also necessary for apoptosis, possibly as an interacting domain with a regulator or a specific substrate.

RICK is another STK recently identified as mediating a specific apoptotic pathway involving the death receptor, CD95 (Inohara, N. et al. (1998) J. Biol. Chem. 273:12296-12300). CD95 is a member of the tumor necrosis factor receptor superfamily and plays a critical role in the regulation 30 and homeostasis of the immune system (Nagata, S. (1997) Cell 88:355-365). The CD95 receptor signaling pathway involves recruitment of various intracellular molecules to a receptor complex following ligand binding. This process includes recruitment of the cysteine protease caspase-8 which, in turn, activates a caspase cascade leading to cell death. RICK is composed of an N-terminal kinase

catalytic domain and a C-terminal "caspase-recruitment" domain that interacts with caspase-like domains, indicating that RICK plays a role in the recruitment of caspase-8. This interpretation is supported by the fact that the expression of RICK in human 293T cells promotes activation of caspase-8 and potentiates the induction of apoptosis by various proteins involved in the CD95 5 apoptosis pathway (Inohara et al. *supra*).

Mitochondrial Protein Kinases

A novel class of eukaryotic kinases, related by sequence to prokaryotic histidine protein kinases, are the mitochondrial protein kinases (MPKs) which seem to have no sequence similarity with other eukaryotic protein kinases. These protein kinases are located exclusively in the mitochondrial 10 matrix space and may have evolved from genes originally present in respiration-dependent bacteria which were endocytosed by primitive eukaryotic cells. MPKs are responsible for phosphorylation and inactivation of the branched-chain alpha-ketoacid dehydrogenase and pyruvate dehydrogenase complexes (Harris, R.A. et al. (1995) *Adv. Enzyme Regul.* 34:147-162). Five MPKs have been identified. Four members correspond to pyruvate dehydrogenase kinase isozymes, regulating the 15 activity of the pyruvate dehydrogenase complex, which is an important regulatory enzyme at the interface between glycolysis and the citric acid cycle. The fifth member corresponds to a branched-chain alpha-ketoacid dehydrogenase kinase, important in the regulation of the pathway for the disposal of branched-chain amino acids. (Harris, R.A. et al. (1997) *Adv. Enzyme Regul.* 37:271-293). Both starvation and the diabetic state are known to result in a great increase in the activity of the pyruvate 20 dehydrogenase kinase in the liver, heart and muscle of the rat. This increase contributes in both disease states to the phosphorylation and inactivation of the pyruvate dehydrogenase complex and conservation of pyruvate and lactate for gluconeogenesis (Harris (1995) *supra*).

KINASES WITH NON-PROTEIN SUBSTRATES

25

Lipid and Inositol kinases

Lipid kinases phosphorylate hydroxyl residues on lipid head groups. A family of kinases involved in phosphorylation of phosphatidylinositol (PI) has been described, each member phosphorylating a specific carbon on the inositol ring (Leevers, S.J. et al. (1999) *Curr. Opin. Cell. Biol.* 30 11:219-225). The phosphorylation of phosphatidylinositol is involved in activation of the protein kinase C signaling pathway. The inositol phospholipids (phosphoinositides) intracellular signaling pathway begins with binding of a signaling molecule to a G-protein linked receptor in the plasma membrane. This leads to the phosphorylation of phosphatidylinositol (PI) residues on the inner side of the plasma

membrane by inositol kinases, thus converting PI residues to the biphosphate state (PIP_2). PIP_2 is then cleaved into inositol triphosphate (IP_3) and diacylglycerol. These two products act as mediators for separate signaling pathways. Cellular responses that are mediated by these pathways are glycogen breakdown in the liver in response to vasopressin, smooth muscle contraction in response to 5 acetylcholine, and thrombin-induced platelet aggregation.

PI 3-kinase (PI3K), which phosphorylates the D3 position of PI and its derivatives, has a central role in growth factor signal cascades involved in cell growth, differentiation, and metabolism. PI3K is a heterodimer consisting of an adapter subunit and a catalytic subunit. The adapter subunit acts as a scaffolding protein, interacting with specific tyrosine-phosphorylated proteins, lipid moieties, 10 and other cytosolic factors. When the adapter subunit binds tyrosine phosphorylated targets, such as the insulin responsive substrate (IRS)-1, the catalytic subunit is activated and converts PI (4,5) bisphosphate (PIP_2) to PI (3,4,5) P_3 (PIP_3). PIP_3 then activates a number of other proteins, including PKA, protein kinase B (PKB), protein kinase C (PKC), glycogen synthase kinase (GSK)-3, and p70 ribosomal s6 kinase. PI3K also interacts directly with the cytoskeletal organizing proteins, Rac, rho, 15 and cdc42 (Shepherd, P.R., et al. (1998) Biochem. J. 333:471-490). Animal models for diabetes, such as *obese* and *fat* mice, have altered PI3K adapter subunit levels. Specific mutations in the adapter subunit have also been found in an insulin-resistant Danish population, suggesting a role for PI3K in type-2 diabetes (*Shepard, supra*).

PKC is also activated by diacylglycerol (DAG). Phorbol esters (PE) are analogs of DAG and 20 tumor promoters that cause a variety of physiological changes when administered to cells and tissues. PE and DAG bind to the N-terminal region of PKC. This region contains one or more copies of a cysteine-rich domain about 50 amino-acid residues long and essential for DAG/PE-binding. Diacylglycerol kinase (DGK), the enzyme that converts DAG into phosphatidate, contains two copies of the DAG/PE-binding domain in its N-terminal section (Azzi, A. et al. (1992) Eur. J. Biochem. 25 208:547-557).

An example of lipid kinase phosphorylation activity is the phosphorylation of 25 D-erythro-sphingosine to the sphingolipid metabolite, sphingosine-1-phosphate (SPP). SPP has emerged as a novel lipid second-messenger with both extracellular and intracellular actions (Kohama, T. et al. (1998) J. Biol. Chem. 273:23722-23728). Extracellularly, SPP is a ligand for the G-protein coupled receptor EDG-1 (endothelial-derived, G-protein coupled receptor). Intracellularly, SPP regulates cell growth, survival, motility, and cytoskeletal changes. SPP levels are regulated by sphingosine kinases that specifically phosphorylate D-erythro-sphingosine to SPP. The importance of sphingosine kinase in cell signaling is indicated by the fact that various stimuli, including

platelet-derived growth factor (PDGF), nerve growth factor, and activation of protein kinase C, increase cellular levels of SPP by activation of sphingosine kinase, and the fact that competitive inhibitors of the enzyme selectively inhibit cell proliferation induced by PDGF (Kohama et al. *supra*).

Purine Nucleotide Kinases

5 The purine nucleotide kinases, adenylate kinase (ATP:AMP phosphotransferase, or AdK) and guanylate kinase (ATP:GMP phosphotransferase, or GuK) play a key role in nucleotide metabolism and are crucial to the synthesis and regulation of cellular levels of ATP and GTP, respectively. These two molecules are precursors in DNA and RNA synthesis in growing cells and provide the primary source of biochemical energy in cells (ATP), and signal transduction pathways (GTP). Inhibition of
10 various steps in the synthesis of these two molecules has been the basis of many antiproliferative drugs for cancer and antiviral therapy (Pillwein, K. et al. (1990) *Cancer Res.* 50:1576-1579).

AdK is found in almost all cell types and is especially abundant in cells having high rates of ATP synthesis and utilization such as skeletal muscle. In these cells AdK is physically associated with mitochondria and myofibrils, the subcellular structures that are involved in energy production and utilization, respectively. Recent studies have demonstrated a major function for AdK in transferring high energy phosphoryls from metabolic processes generating ATP to cellular components consuming ATP (Zeleznikar, R.J. et al. (1995) *J. Biol. Chem.* 270:7311-7319). Thus AdK may have a pivotal role in maintaining energy production in cells, particularly those having a high rate of growth or metabolism such as cancer cells, and may provide a target for suppression of its activity to treat
15 certain cancers. Alternatively, reduced AdK activity may be a source of various metabolic, muscle-energy disorders that can result in cardiac or respiratory failure and may be treatable by increasing AdK activity.

GuK, in addition to providing a key step in the synthesis of GTP for RNA and DNA synthesis, also fulfills an essential function in signal transduction pathways of cells through the regulation of GDP
25 and GTP. Specifically, GTP binding to membrane associated G proteins mediates the activation of cell receptors, subsequent intracellular activation of adenyl cyclase, and production of the second messenger, cyclic AMP. GDP binding to G proteins inhibits these processes. GDP and GTP levels also control the activity of certain oncogenic proteins such as p21^{ras} known to be involved in control of cell proliferation and oncogenesis (Bos, J.L. (1989) *Cancer Res.* 49:4682-4689). High ratios of
30 GTP:GDP caused by suppression of GuK cause activation of p21^{ras} and promote oncogenesis. Increasing GuK activity to increase levels of GDP and reduce the GTP:GDP ratio may provide a therapeutic strategy to reverse oncogenesis.

GuK is an important enzyme in the phosphorylation and activation of certain antiviral drugs

useful in the treatment of herpes virus infections. These drugs include the guanine homologs acyclovir and buciclovir (Miller, W.H. and Miller R.L. (1980) J. Biol. Chem. 255:7204-7207; Stenberg, K. et al. (1986) J. Biol. Chem. 261:2134-2139). Increasing GuK activity in infected cells may provide a therapeutic strategy for augmenting the effectiveness of these drugs and possibly for reducing the
5 necessary dosages of the drugs.

Pyrimidine Kinases

The pyrimidine kinases are deoxycytidine kinase and thymidine kinase 1 and 2. Deoxycytidine kinase is located in the nucleus, and thymidine kinase 1 and 2 are found in the cytosol (Johansson, M. et al. (1997) Proc. Natl. Acad. Sci. U.S.A. 94:11941-11945). Phosphorylation of
10 deoxyribonucleosides by pyrimidine kinases provides an alternative pathway for de novo synthesis of DNA precursors. The role of pyrimidine kinases, like purine kinases, in phosphorylation is critical to the activation of several chemotherapeutically important nucleoside analogues (Arner E.S. and Eriksson, S. (1995) Pharmacol. Ther. 67:155-186).

The discovery of new human kinases, and the polynucleotides encoding them, satisfies a need
15 in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of human kinases.

20

SUMMARY OF THE INVENTION

The invention features purified polypeptides, human kinases, referred to collectively as "PKIN" and individually as "PKIN-1," "PKIN-2," "PKIN-3," "PKIN-4," "PKIN-5," "PKIN-6," "PKIN-7," "PKIN-8," "PKIN-9," "PKIN-10," "PKIN-11," "PKIN-12," "PKIN-13," "PKIN-14," "PKIN-15," "PKIN-16," "PKIN-17," "PKIN-18," "PKIN-19," "PKIN-20," "PKIN-21," and "PKIN-22." In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of
25 SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-22.
30

The invention further provides an isolated polynucleotide encoding a polypeptide selected from

the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-22. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:23-44.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an

amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

- The invention further provides an isolated polynucleotide selected from the group consisting of
- 5 a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44,
 - 10 c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of

- a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 15 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44,
- c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to
- 20 said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of

- a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the 30 polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the

invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

5 The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide
10 10 having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

15 The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, c) a biologically active fragment of a polypeptide
20 20 having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the
25 25 polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a
30 30 polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said

method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, ii) a 5 polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological 10 sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the polynucleotide of 15 ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of 20 toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the present invention.

25 Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog for polypeptides of the invention. The probability score for the match between each polypeptide and its GenBank homolog is also shown.

Table 3 shows structural features of polypeptide sequences of the invention, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for 30 analysis of the polypeptides.

Table 4 lists the cDNA and/or genomic DNA fragments which were used to assemble polynucleotide sequences of the invention, along with selected fragments of the polynucleotide sequences.

Table 5 shows the representative cDNA library for polynucleotides of the invention.

Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

Table 7 shows the tools, programs, and algorithms used to analyze the polynucleotides and 5 polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these 10 may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a 15 reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. 20 Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the 25 invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"PKIN" refers to the amino acid sequences of substantially purified PKIN obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

30 The term "agonist" refers to a molecule which intensifies or mimics the biological activity of PKIN. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of PKIN either by directly interacting with PKIN or by acting on components of the biological pathway in which PKIN participates.

An "allelic variant" is an alternative form of the gene encoding PKIN. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to 5 allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding PKIN include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as PKIN or a 10 polypeptide with at least one functional characteristic of PKIN. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding PKIN, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding PKIN. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino 15 acid residues which produce a silent change and result in a functionally equivalent PKIN. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of PKIN is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and 20 arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, 25 polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. 30 Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of PKIN. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small

molecules, or any other compound or composition which modulates the activity of PKIN either by directly interacting with PKIN or by acting on components of the biological pathway in which PKIN participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind PKIN polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "aptamer" refers to a nucleic acid or oligonucleotide molecule that binds to a specific molecular target. Aptamers are derived from an *in vitro* evolutionary process (e.g., SELEX (Systematic Evolution of Ligands by EXponential Enrichment), described in U.S. Patent No. 5,270,163), which selects for target-specific aptamer sequences from large combinatorial libraries. Aptamer compositions may be double-stranded or single-stranded, and may include deoxyribonucleotides, ribonucleotides, nucleotide derivatives, or other nucleotide-like molecules. The nucleotide components of an aptamer may have modified sugar groups (e.g., the 2'-OH group of a ribonucleotide may be replaced by 2'-F or 2'-NH₂), which may improve a desired property, e.g., resistance to nucleases or longer lifetime in blood. Aptamers may be conjugated to other molecules, e.g., a high molecular weight carrier to slow clearance of the aptamer from the circulatory system. Aptamers may be specifically cross-linked to their cognate ligands, e.g., by photo-activation of a cross-linker. (See, e.g., Brody, E.N. and L. Gold (2000) J. Biotechnol. 74:5-13.)

The term "intramer" refers to an aptamer which is expressed *in vivo*. For example, a vaccinia virus-based RNA expression system has been used to express specific RNA aptamers at high levels in the cytoplasm of leukocytes (Blind, M. et al. (1999) Proc. Natl Acad. Sci. USA 96:3606-3610).

The term "spiegelmer" refers to an aptamer which includes L-DNA, L-RNA, or other left-

handed nucleotide derivatives or nucleotide-like molecules. Aptamers containing left-handed nucleotides are resistant to degradation by naturally occurring enzymes, which normally act on substrates containing right-handed nucleotides.

The term "antisense" refers to any composition capable of base-pairing with the "sense" 5 (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense 10 molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

15 The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic PKIN, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

20 "Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or 25 amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding PKIN or fragments of PKIN may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; 30 SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been

assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

5 "Conservative amino acid substitutions" are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
10	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
15	Cys	Ala, Ser
	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
20	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
25	Ser	Cys, Thr
	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr
30		

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

35 A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains 40 at least one biological or immunological function of the natural molecule. A derivative polypeptide is

one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

5 "Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

10 "Exon shuffling" refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

15 A "fragment" is a unique portion of PKIN or the polynucleotide encoding PKIN which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For 20 example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

25 A fragment of SEQ ID NO:23-44 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:23-44, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:23-44 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:23-44 from related polynucleotide sequences. The precise length of a fragment of SEQ ID 30 NO:23-44 and the region of SEQ ID NO:23-44 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-22 is encoded by a fragment of SEQ ID NO:23-44. A fragment of SEQ ID NO:1-22 comprises a region of unique amino acid sequence that specifically

identifies SEQ ID NO:1-22. For example, a fragment of SEQ ID NO:1-22 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-22. The precise length of a fragment of SEQ ID NO:1-22 and the region of SEQ ID NO:1-22 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the 5 intended purpose for the fragment.

A "full length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two 10 or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore 15 achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in 20 Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

25 Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis 30 programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The

"BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

5 *Matrix: BLOSUM62*

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

10 *Expect: 10*

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, 15 over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

20 Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to 25 the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

30 Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap

penalty=3, window=5, and “diagonals saved”=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the “BLAST 2 Sequences” tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

10 *Gap x drop-off: 50*

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, 15 for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be 20 used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term ‘humanized antibody’ refers to an antibody molecule in which the amino acid 25 sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. 30 Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the “washing” step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive

conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 5 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of 10 the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention 15 include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking 20 reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency 25 conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid 30 sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., $C_{0,t}$ or $R_{0,t}$ analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate 35 to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively. "Immune response" can refer to conditions associated with inflammation, trauma, immune

disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of PKIN which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of PKIN which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

10 The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of PKIN. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of PKIN.

15 The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

20 "Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

25 "Post-translational modification" of an PKIN may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of PKIN.

30 "Probe" refers to nucleic acid sequences encoding PKIN, their complements, or fragments

thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target 5 polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also 10 be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for 15 example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that 20 purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 25 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer 30 selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may

also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, *supra*. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing PKIN, nucleic acids encoding PKIN, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

- 5 The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the
10 epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

15 The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

20 "Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

25 "Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed
30 cells" includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "transgenic organism," as used herein, is any organism, including but not limited to animals

and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation.

10 Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

30 A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at

least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

5 THE INVENTION

The invention is based on the discovery of new human kinases (PKIN), the polynucleotides encoding PKIN, and the use of these compositions for the diagnosis, treatment, or prevention of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders.

10 Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is
15 denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

Table 2 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (genpept) database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte 20 polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (Genbank ID NO:) of the nearest GenBank homolog. Column 4 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 5 shows the annotation of the GenBank homolog along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

25 Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS 30 program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI). Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are human kinases.

For example, SEQ ID NO:1 is 91% identical to human casein kinase I-alpha (GenBank ID g852055) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The 5 BLAST probability score is 2.9e-167, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:1 also contains a eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ 10 ID NO:1 is a protein kinase.

For example, SEQ ID NO:10 is 91% identical to Mus musculus FYVE finger-containing phosphoinositide kinase (GenBank ID g4200446) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:10 also contains a 15 phosphatidyl inositol 4-phosphate 5-kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from PRODOM analysis provides further corroborative evidence that SEQ ID NO:10 is a phosphoinositide kinase.

For example, SEQ ID NO:12 is 71% identical to human serine/threonine protein kinase 20 (GenBank ID g7160989) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 1.7e-148, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:12 also contains a eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden 25 Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS and MOTIFS analyses provide further corroborative evidence that SEQ ID NO:12 is protein kinase.

For example, SEQ ID NO:13 is 86% identical to murine pantothenate kinase 1 beta (GenBank ID g6690020) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 1.6e-129, which indicates the probability of obtaining the observed 30 polypeptide sequence alignment by chance. Pantothenate kinase (PanK) is proposed to be the master regulator of CoA biosynthesis in mammalian cells, by controlling flux through the CoA biosynthetic pathway. Changes in the level of tissue PanK activity is reflected by the concurrent changes in the levels of CoA as seen in various metabolic states. Alterations in CoA levels and PanK activity are

seen during starvation/feeding, pathological states such as diabetes and by treatment with hypolipidemic drugs (Rock, C.O. et al., (2000) J. Biol. Chem. 275:1377-1383.)

For example, SEQ ID NO:16 is 68% identical to Mus musculus Nck-interacting kinase-like embryo specific kinase (GenBank ID g6472874) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:16 also contains a eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:16 is a protein kinase.

For example, SEQ ID NO:19 is 99% identical to human RET tyrosine kinase receptor (GenBank ID g5419753) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:19 also contains a eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:19 is a tyrosine kinase.

For example, SEQ ID NO:22 is 33% identical to *Gallus gallus* smooth muscle myosin light chain kinase precursor (GenBank ID g212661) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 1.2 e-60, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:22 also contains two eukaryotic protein kinase domains as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:22 is a protein kinase.

SEQ ID NO:2-9, SEQ ID NO:11, SEQ ID NO:14-15, SEQ ID NO:17-18, and SEQ ID NO:20-21 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-22 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide

consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:23-44 or that distinguish between SEQ ID NO:23-44 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 183812R7 is the identification number of an Incyte cDNA sequence, and CARDNOT01 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 71583296V1). Alternatively, the identification numbers in column 5 may refer to GenBank cDNAs or ESTs which contributed to the assembly of the full length polynucleotide sequences. In addition, the identification numbers in column 5 may identify sequences derived from the ENSEMBL (The Sanger Centre, Cambridge, UK) database (*i.e.*, those sequences including the designation “ENST”). Alternatively, the identification numbers in column 5 may be derived from the NCBI RefSeq Nucleotide Sequence Records Database (*i.e.*, those sequences including the designation “NM” or “NT”) or the NCBI RefSeq Protein Sequence Records (*i.e.*, those sequences including the designation “NP”). Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an “exon stitching” algorithm. For example, FL_XXXXXX_N₁_N₂_YYYYY_N₃_N₄ represents a “stitched” sequence in which XXXXXX is the identification number of the cluster of sequences to which the algorithm was applied, and YYYY is the number of the prediction generated by the algorithm, and N_{1,2,3...}, if present, represent specific exons that may have been manually edited during analysis (See Example V). Alternatively, the identification numbers in column 5 may refer to assemblages of exons brought together by an “exon-stretching” algorithm. For example, FLXXXXX_gAAAAAA_gBBBBB_1_N is the identification number of a “stretched” sequence, with XXXXXX being the Incyte project identification number, gAAAAAA being the GenBank identification number of the human genomic sequence to which the “exon-stretching” algorithm was applied, gBBBBB being the GenBank identification number or NCBI RefSeq identification number of the nearest GenBank protein homolog, and N referring to

specific exons (See Example V). In instances where a RefSeq sequence was used as a protein homolog for the “exon-stretching” algorithm, a RefSeq identifier (denoted by “NM,” “NP,” or “NT”) may be used in place of the GenBank identifier (*i.e.*, gBBBBB).

Alternatively, a prefix identifies component sequences that were hand-edited, predicted from 5 genomic DNA sequences, or derived from a combination of sequence analysis methods. The following Table lists examples of component sequence prefixes and corresponding sequence analysis methods associated with the prefixes (see Example IV and Example V).

Prefix	Type of analysis and/or examples of programs
GNN, GFG, ENST	Exon prediction from genomic sequences using, for example, GENSCAN (Stanford University, CA, USA) or FGENES (Computer Genomics Group, The Sanger Centre, Cambridge, UK)
GBI	Hand-edited analysis of genomic sequences.
FL	Stitched or stretched genomic sequences (see Example V).
INCY	Full length transcript and exon prediction from mapping of EST sequences to the genome. Genomic location and EST composition data are combined to predict the exons and resulting transcript.

15 In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in column 5 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotide sequences which were assembled using Incyte cDNA sequences. The representative cDNA library 20 is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to assemble and confirm the above polynucleotide sequences. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

The invention also encompasses PKIN variants. A preferred PKIN variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid 25 sequence identity to the PKIN amino acid sequence, and which contains at least one functional or structural characteristic of PKIN.

The invention also encompasses polynucleotides which encode PKIN. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:23-44, which encodes PKIN. The polynucleotide sequences 30 of SEQ ID NO:23-44, as presented in the Sequence Listing, embrace the equivalent RNA sequences,

wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding PKIN. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least 5 about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding PKIN. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:23-44 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% 10 polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:23-44. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of PKIN.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding PKIN, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, 15 the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring PKIN, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode PKIN and its variants are generally capable of 20 hybridizing to the nucleotide sequence of the naturally occurring PKIN under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding PKIN or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which 25 particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding PKIN and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode PKIN and 30 PKIN derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding PKIN or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:23-44 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A.R. (1987) Methods Enzymol. 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

- Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)
- The nucleic acid sequences encoding PKIN may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.)
- Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060).

Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode PKIN may be cloned in recombinant DNA molecules that direct expression of PKIN, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express PKIN.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter PKIN-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent No. 5,837,458; Chang, C.-C. et al. (1999) *Nat. Biotechnol.* 17:793-797; Christians, F.C. et al. (1999) *Nat. Biotechnol.* 17:259-264; and Crameri, A. et al. (1996) *Nat. Biotechnol.* 14:315-319) to alter or improve 5 the biological properties of PKIN, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and 10 selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple 15 naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding PKIN may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) *Nucleic Acids Symp. Ser.* 7:215-223; and Horn, T. et al. (1980) *Nucleic Acids Symp. Ser.* 7:225-232.) Alternatively, 20 PKIN itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) *Proteins, Structures and Molecular Properties*, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) *Science* 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence 25 of PKIN, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. 30 (See, e.g., Creighton, *supra*, pp. 28-53.)

In order to express a biologically active PKIN, the nucleotide sequences encoding PKIN or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in

a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding PKIN. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding PKIN. Such signals 5 include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding PKIN and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided 10 by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression 15 vectors containing sequences encoding PKIN and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

20 A variety of expression vector/host systems may be utilized to contain and express sequences encoding PKIN. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or 25 tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509; Engelhard, E.K. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:3224-3227; Sandig, V. et al. (1996) *Hum. Gene Ther.* 7:1937-1945; Takamatsu, N. (1987) *EMBO J.* 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New 30 York NY, pp. 191-196; Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659; and Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola,

M. et al. (1998) *Cancer Gen. Ther.* 5(6):350-356; Yu, M. et al. (1993) *Proc. Natl. Acad. Sci. USA* 90(13):6340-6344; Buller, R.M. et al. (1985) *Nature* 317(6040):813-815; McGregor, D.P. et al. (1994) *Mol. Immunol.* 31(3):219-226; and Verma, I.M. and N. Somia (1997) *Nature* 389:239-242.) The invention is not limited by the host cell employed.

5 In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding PKIN. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding PKIN can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding PKIN into the vector's multiple cloning 10 site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for *in vitro* transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509.) When large quantities of PKIN are needed, e.g. for the production of 15 antibodies, vectors which direct high level expression of PKIN may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of PKIN. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such 20 vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; and Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184.)

Plant systems may also be used for expression of PKIN. Transcription of sequences 25 encoding PKIN may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105.) These 30 constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases

where an adenovirus is used as an expression vector, sequences encoding PKIN may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses PKIN in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of PKIN in cell lines is preferred. For example, sequences encoding PKIN can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* and *apr* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate

luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) *Methods Mol. Biol.* 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding PKIN is inserted within a marker gene sequence, transformed cells containing sequences encoding PKIN can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding PKIN under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding PKIN and that express PKIN may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of PKIN using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on PKIN is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) *Serological Methods, a Laboratory Manual*, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) *Current Protocols in Immunology*, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) *Immunochemical Protocols*, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding PKIN include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding PKIN, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety

of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

5 Host cells transformed with nucleotide sequences encoding PKIN may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode PKIN may be designed to contain signal sequences which direct
10 secretion of PKIN through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the
15 protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

20 In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding PKIN may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric PKIN protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of PKIN activity. Heterologous protein and
25 peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins,
30 respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the PKIN encoding sequence and the heterologous protein sequence, so that PKIN

may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, *supra*, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled PKIN may be achieved *in vitro* using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ^{35}S -methionine.

PKIN of the present invention or fragments thereof may be used to screen for compounds that specifically bind to PKIN. At least one and up to a plurality of test compounds may be screened for specific binding to PKIN. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of PKIN, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) *Current Protocols in Immunology* 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which PKIN binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express PKIN, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing PKIN or cell membrane fractions which contain PKIN are then contacted with a test compound and binding, stimulation, or inhibition of activity of either PKIN or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with PKIN, either in solution or affixed to a solid support, and detecting the binding of PKIN to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

PKIN of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of PKIN. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for PKIN

activity, wherein PKIN is combined with at least one test compound, and the activity of PKIN in the presence of a test compound is compared with the activity of PKIN in the absence of the test compound. A change in the activity of PKIN in the presence of the test compound is indicative of a compound that modulates the activity of PKIN. Alternatively, a test compound is combined with an in vitro or cell-free system comprising PKIN under conditions suitable for PKIN activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of PKIN may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

- In another embodiment, polynucleotides encoding PKIN or their mammalian homologs may be
- 10 "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent No. 5,175,383 and U.S. Patent No. 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted
- 15 by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330).
- 20 Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding PKIN may also be manipulated in vitro in ES cells derived from

25 human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding PKIN can also be used to create "knockin" humanized animals

30 (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding PKIN is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with

potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress PKIN, e.g., by secreting PKIN in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

- 5 Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of PKIN and human kinases. In addition, the expression of PKIN is closely associated with brain, breast tumor, cardiovascular, digestive, fallopian tube tumor, fetal stomach, nervous, ovarian tumor, pancreatic tumor, peritoneal tumor, pituitary gland, placental, prostate tumor, neural, spinal cord, and testicular tissues, and with umbilical cord blood dendritic cells. Therefore, PKIN appears to play a
10 role in cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders. In the treatment of disorders associated with increased PKIN expression or activity, it is desirable to decrease the expression or activity of PKIN. In the treatment of disorders associated with decreased PKIN expression or activity, it is desirable to increase the expression or activity of PKIN.
- 15 Therefore, in one embodiment, PKIN or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN. Examples of such disorders include, but are not limited to, a cancer, such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia,
20 gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, leukemias such as multiple myeloma, and lymphomas such as Hodgkin's disease; an immune disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune
25 thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis,
30 myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral,

bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a growth and developmental disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including

5 adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy,

10 gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and

15 sensorineural hearing loss; a cardiovascular disease, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease,

20 degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung

25 anomalies; atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic

30 pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and

noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a lipid disorder such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such Fabry's
5 disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, lipodystrophy, lipomatoses, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipoid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia,
10 primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, lipid myopathies, and obesity.

15 In another embodiment, a vector capable of expressing PKIN or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified PKIN in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN including, but not limited to, those provided above.

20 In still another embodiment, an agonist which modulates the activity of PKIN may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN including, but not limited to, those listed above.

25 In a further embodiment, an antagonist of PKIN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PKIN. Examples of such disorders include, but are not limited to, those cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders described above. In one aspect, an antibody which specifically binds PKIN may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express PKIN.

30 In an additional embodiment, a vector expressing the complement of the polynucleotide encoding PKIN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PKIN including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary

sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the 5 various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of PKIN may be produced using methods which are generally known in the art. In particular, purified PKIN may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind PKIN. Antibodies to PKIN may also 10 be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and 15 others may be immunized by injection with PKIN or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG 20 (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to PKIN have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of PKIN 25 amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to PKIN may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma 30 technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the

splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce PKIN-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population 10 or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for PKIN may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin 15 digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired 20 specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between PKIN and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering PKIN epitopes is generally used, but a competitive binding assay may also be 25 employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for PKIN. Affinity is expressed as an association constant, K_a, which is defined as the molar concentration of PKIN-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a 30 determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple PKIN epitopes, represents the average affinity, or avidity, of the antibodies for PKIN. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular PKIN epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a

ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the PKIN-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_d ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of PKIN, preferably in active form, from the antibody

5 (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a

10 polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of PKIN-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

15 In another embodiment of the invention, the polynucleotides encoding PKIN, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding PKIN. Such technology is well known in the art, and antisense oligonucleotides or larger fragments

20 can be designed from various locations along the coding or control regions of sequences encoding PKIN. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totowa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence

25 complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other

30 gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

- In another embodiment of the invention, polynucleotides encoding PKIN may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined 5 immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassamias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, 10 R.G. (1995) *Science* 270:404-410; Verma, I.M. and N. Somia (1997) *Nature* 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) *Nature* 335:395-396; Poeschla, E. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:11395-11399), 15 hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in PKIN expression or regulation causes disease, the expression of PKIN from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.
- 20 In a further embodiment of the invention, diseases or disorders caused by deficiencies in PKIN are treated by constructing mammalian expression vectors encoding PKIN and introducing these vectors by mechanical means into PKIN-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and 25 (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) *Annu. Rev. Biochem.* 62:191-217; Ivics, Z. (1997) *Cell* 91:501-510; Boulay, J-L. and H. Récipon (1998) *Curr. Opin. Biotechnol.* 9:445-450).

- Expression vectors that may be effective for the expression of PKIN include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX, PCR2-TOPOTA vectors 30 (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA); and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). PKIN may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β-actin genes), (ii) an inducible promoter

(e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) Proc. Natl. Acad. Sci. USA 89:5547-5551; Gossen, M. et al. (1995) Science 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the 5 FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding PKIN from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver 10 polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al. (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to PKIN expression are treated by constructing a retrovirus vector consisting of (i) the 15 polynucleotide encoding PKIN under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences 20 required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. USA 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. 25 (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and A.D. Miller (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent No. 5,910,434 to Rigg ("Method for obtaining 30 retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998)

Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

- In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding PKIN to cells which have one or more genetic abnormalities with respect to the expression of PKIN. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent No. 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and N. Somia (1997) Nature 389:239-242, both incorporated by reference herein.

- In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding PKIN to target cells which have one or more genetic abnormalities with respect to the expression of PKIN. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing PKIN to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent No. 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent No. 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding PKIN to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based

on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity 5 (e.g., protease and polymerase). Similarly, inserting the coding sequence for PKIN into the alphavirus genome in place of the capsid-coding region results in the production of a large number of PKIN-coding RNAs and the synthesis of high levels of PKIN in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that 10 the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of PKIN into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating 15 infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfactions, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, 20 transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

25 Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding PKIN.

30 Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for

secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared
5 by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding PKIN. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs
10 that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages
15 within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a
20 compound which is effective in altering expression of a polynucleotide encoding PKIN. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective
25 compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased PKIN expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding PKIN may be therapeutically useful, and in the treatment of disorders associated with decreased PKIN expression or activity, a compound which specifically promotes expression of the
30 polynucleotide encoding PKIN may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in

altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a

5 polynucleotide encoding PKIN is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding PKIN are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the

10 polynucleotide encoding PKIN. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide

15 can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified

20 oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruice, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruice, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient.

25 Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and

30 monkeys.

An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various

formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of PKIN, antibodies to PKIN, and mimetics, agonists, antagonists, or inhibitors of PKIN.

The compositions utilized in this invention may be administered by any number of routes
5 including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form.
These compositions are generally aerosolized immediately prior to inhalation by the patient. In the
10 case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without
15 needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

Specialized forms of compositions may be prepared for direct intracellular delivery of
20 macromolecules comprising PKIN or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, PKIN or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et
25 al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for
30 administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example PKIN or fragments thereof, antibodies of PKIN, and agonists, antagonists or inhibitors of PKIN, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by

standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED₅₀ (the dose therapeutically effective in 50% of the population) or LD₅₀ (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD₅₀/ED₅₀ ratio. Compositions which exhibit large 5 therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED₅₀ with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

10 The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response 15 to therapy. Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 µg to 100,000 µg, up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. 20 Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind PKIN may be used for the 25 diagnosis of disorders characterized by expression of PKIN, or in assays to monitor patients being treated with PKIN or agonists, antagonists, or inhibitors of PKIN. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for PKIN include methods which utilize the antibody and a label to detect PKIN in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and 30 may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring PKIN, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of PKIN expression. Normal

or standard values for PKIN expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to PKIN under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of PKIN expressed in subject, 5 control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding PKIN may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect 10 and quantify gene expression in biopsied tissues in which expression of PKIN may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of PKIN, and to monitor regulation of PKIN levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding PKIN or closely related molecules may be used to 15 identify nucleic acid sequences which encode PKIN. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding PKIN, allelic variants, or related sequences.

20 Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the PKIN encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:23-44 or from genomic sequences including promoters, enhancers, and introns of the PKIN gene.

Means for producing specific hybridization probes for DNAs encoding PKIN include the 25 cloning of polynucleotide sequences encoding PKIN or PKIN derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, 30 such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding PKIN may be used for the diagnosis of disorders associated with expression of PKIN. Examples of such disorders include, but are not limited to, a cancer, such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma,

teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, leukemias such as multiple myeloma and lymphomas such as Hodgkin's disease; an immune disorder,
5 such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins,
10 erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis,
15 thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a growth and developmental disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and
20 cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker
25 muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly,
30 craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss; a cardiovascular disease, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary

artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic

5 endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary

10 disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary

15 hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a lipid disorder such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid

20 storage disorders such Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, lipodystrophy, lipomatoses, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipoid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with

25 hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, lipid myopathies, and obesity. The polynucleotide sequences encoding PKIN may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick,

30 pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered PKIN expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding PKIN may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide

sequences encoding PKIN may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding PKIN in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

- In order to provide a basis for the diagnosis of a disorder associated with expression of PKIN,
- 10 a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding PKIN, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used.
- 15 Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

- Once the presence of a disorder is established and a treatment protocol is initiated,
- hybridization assays may be repeated on a regular basis to determine if the level of expression in the
- 20 patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

- With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development
- 25 of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

- Additional diagnostic uses for oligonucleotides designed from the sequences encoding PKIN
- 30 may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding PKIN, or a fragment of a polynucleotide complementary to the polynucleotide encoding PKIN, and will be employed under optimized conditions for identification of a specific gene or

condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding PKIN may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding PKIN are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed *in silico* SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of PKIN include radiolabeling or biotinylation of nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor

progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and 5 display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, PKIN, fragments of PKIN, or antibodies specific for PKIN may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

10 A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent No. 15 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the 20 hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention 25 may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) 30 Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression

provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

10 In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for

example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for PKIN to quantify the levels of PKIN expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lucking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendoza, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the

two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding PKIN may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, for example, Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding PKIN on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery

techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) *Nature* 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, PKIN, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between PKIN and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with PKIN, or fragments thereof, and washed. Bound PKIN is then detected by methods well known in the art. Purified PKIN can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding PKIN specifically compete with a test compound for binding PKIN. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PKIN.

In additional embodiments, the nucleotide sequences which encode PKIN may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific

embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/242,410, U.S. Ser. No. 60/244,068, U.S. Ser. No. 60/245,708, U.S. Ser. 5 No. 60/247,672, U.S. Ser. No. 60/249,565, U.S. Ser. No. 60/252,730, and U.S. Ser. No. 60/250,807, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

10 Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA) and shown in Table 4, column 5. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl 15 cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles 20 (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the 25 UNIZAP vector system (Stratagene) or SUPERSCRIPT plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, *supra*, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300- 30 1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid

(Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), PCR2-TOPOTA plasmid (Invitrogen), PCMV-ICIS plasmid (Stratagene), pIGEN (Incyte Genomics, Palo Alto CA), or pINCY (Incyte Genomics), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or

- 5 ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an

- 10 AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4 °C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSCAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

20 III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the 25 MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the 30 ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, unit 7.7). Some of the cDNA sequences were selected for extension using the

techniques disclosed in Example VIII.

- The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The
- 5 Incyte cDNA sequences or translations thereof were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.)
- 10 The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and
- 15 Consed, and cDNA assemblages were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein
- 20 databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden Markov model (HMM)-based protein family databases such as PFAM. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as
- 25 incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second

30 column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the

identity between two sequences).

The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:23-44. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and
5 amplification technologies are described in Table 4, column 4.

IV. Identification and Editing of Coding Sequences from Genomic DNA

Putative human kinases were initially identified by running the Genscan gene identification program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of
10 organisms (See Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94, and Burge, C. and S. Karlin (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA
15 sequences encode human kinases, the encoded polypeptides were analyzed by querying against PFAM models for human kinases. Potential human kinases were also identified by homology to Incyte cDNA sequences that had been annotated as human kinases. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpri public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to
20 the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted
25 coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

"Stitched" Sequences

30 Partial cDNA sequences were extended with exons predicted by the Genscan gene identification program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm

based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence. Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to 5 be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then "stitched" together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants.

10 Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbpri public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended 15 with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

"Stretched" Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases 20 using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The 25 GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore "stretched" or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

VI. Chromosomal Mapping of PKIN Encoding Polynucleotides

30 The sequences which were used to assemble SEQ ID NO:23-44 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:23-44 were assembled into clusters of contiguous and overlapping sequences using

assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment 5 of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in 10 humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease 15 genes map within or in proximity to the intervals indicated above.

In this manner, SEQ ID NO:29 was mapped to chromosome 1 within the interval from 199.20 to 203.00 centiMorgans, to chromosome 13 within the interval from 105.20 centiMorgans to the q terminus, and to chromosome 6 within the interval from 59.60 to 72.20 centiMorgans. More than one map location is reported for SEQ ID NO:29, indicating that sequences having different map locations 20 were assembled into a single cluster. This situation occurs, for example, when sequences having strong similarity, but not complete identity, are assembled into a single cluster.

VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs 25 from a particular cell type or tissue have been bound. (See, e.g., Sambrook, *supra*, ch. 7; Ausubel (1995) *supra*, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer 30 search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

BLAST Score x Percent Identity
5 x minimum {length(Seq. 1), length(Seq. 2)}

The product score takes into account both the degree of similarity between two sequences and the
5 length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by
10 gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the
15 other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotide sequences encoding PKIN are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA
20 sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or
25 urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and
30 disease-specific expression of cDNA encoding PKIN. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VIII. Extension of PKIN Encoding Polynucleotides

Full length polynucleotide sequences were also produced by extension of an appropriate

fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was synthesized to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg²⁺, (NH₄)₂SO₄, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector

(Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

5 The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA 10 recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, full length polynucleotide sequences are verified using the above procedure or 15 are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:23-44 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base 20 pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 µCi of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a 25 SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon 30 membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and

compared.

X. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, *supra*.), mechanical 5 microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Schena (1999), *supra*). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may 10 be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., Schena, M. et al. (1995) *Science* 270:467-470; Shalon, D. et al. (1996) *Genome Res.* 6:639-645; Marshall, A. and J. Hodgson (1998) *Nat. Biotechnol.* 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may 15 comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a 20 fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

25 Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M 30 dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by *in vitro* transcription from non-coding yeast genomic DNA. After incubation at 37°C for 2 hr, each reaction sample (one

with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated 5 using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 µl 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element 10 is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 µg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope 15 slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

20 Array elements are applied to the coated glass substrate using a procedure described in U.S. Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). 25 Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

30 Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly

larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μ l of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

5 Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide 10 containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, 15 Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

20 The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, 25 are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC 30 computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission

spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used
5 for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XI. Complementary Polynucleotides

Sequences complementary to the PKIN-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring PKIN. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with
10 smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of PKIN. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the PKIN-encoding transcript.

15 XII. Expression of PKIN

Expression and purification of PKIN is achieved using bacterial or virus-based expression systems. For expression of PKIN in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid
20 promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express PKIN upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of PKIN in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly
25 known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding PKIN by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the
30 latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, PKIN is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step,

affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from PKIN at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified PKIN obtained by these methods can be used directly in the assays shown in Examples XVI, XVII, and XVIII, where applicable.

XIII. Functional Assays

PKIN function is assessed by expressing the sequences encoding PKIN at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of PKIN on gene expression can be assessed using highly purified populations

of cells transfected with sequences encoding PKIN and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding PKIN and other genes of interest can be analyzed by northern analysis or microarray techniques.

15 **XIV. Production of PKIN Specific Antibodies**

PKIN substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) Methods Enzymol. 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

20 Alternatively, the PKIN amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-PKIN activity by, for example, binding the peptide or PKIN to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

25 **XV. Purification of Naturally Occurring PKIN Using Specific Antibodies**

Naturally occurring or recombinant PKIN is substantially purified by immunoaffinity chromatography using antibodies specific for PKIN. An immunoaffinity column is constructed by covalently coupling anti-PKIN antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is 30 blocked and washed according to the manufacturer's instructions.

Media containing PKIN are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PKIN (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt

antibody/PKIN binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and PKIN is collected.

XVI. Identification of Molecules Which Interact with PKIN

- PKIN, or biologically active fragments thereof, are labeled with ^{125}I Bolton-Hunter reagent.
- 5 (See, e.g., Bolton, A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled PKIN, washed, and any wells with labeled PKIN complex are assayed. Data obtained using different concentrations of PKIN are used to calculate values for the number, affinity, and association of PKIN with the candidate molecules.
- 10 Alternatively, molecules interacting with PKIN are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech). PKIN may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions
- 15 between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XVII. Demonstration of PKIN Activity

- Generally, protein kinase activity is measured by quantifying the phosphorylation of a protein substrate by PKIN in the presence of gamma-labeled ^{32}P -ATP. PKIN is incubated with the protein substrate, ^{32}P -ATP, and an appropriate kinase buffer. The ^{32}P incorporated into the substrate is separated from free ^{32}P -ATP by electrophoresis and the incorporated ^{32}P is counted using a radioisotope counter. The amount of incorporated ^{32}P is proportional to the activity of PKIN. A determination of the specific amino acid residue phosphorylated is made by phosphoamino acid analysis of the hydrolyzed protein.

- In one alternative, protein kinase activity is measured by quantifying the transfer of gamma phosphate from adenosine triphosphate (ATP) to a serine, threonine or tyrosine residue in a protein substrate. The reaction occurs between a protein kinase sample with a biotinylated peptide substrate and gamma ^{32}P -ATP. Following the reaction, free avidin in solution is added for binding to the 30 biotinylated ^{32}P -peptide product. The binding sample then undergoes a centrifugal ultrafiltration process with a membrane which will retain the product-avidin complex and allow passage of free gamma ^{32}P -ATP. The reservoir of the centrifuged unit containing the ^{32}P -peptide product as retentate is then counted in a scintillation counter. This procedure allows assay of any type of protein kinase

sample, depending on the peptide substrate and kinase reaction buffer selected. This assay is provided in kit form (ASUA, Affinity Ultrafiltration Separation Assay, Transbio Corporation, Baltimore MD, U.S. Patent No. 5,869,275). Suggested substrates and their respective enzymes are as follows:

Histone H1 (Sigma) and p34^{cdc2}kinase, Annexin I, Angiotensin (Sigma) and EGF receptor kinase,

5 Annexin II and *src* kinase, ERK1 & ERK2 substrates and MEK, and myelin basic protein and ERK (Pearson, J.D. et al. (1991) Methods in Enzymology 200:62-81).

In another alternative, protein kinase activity of PKIN is demonstrated *in vitro* in an assay containing PKIN, 50µl of kinase buffer, 1µg substrate, such as myelin basic protein (MBP) or synthetic peptide substrates, 1 mM DTT, 10 µg ATP, and 0.5µCi [γ -³³P]ATP. The reaction is

10 incubated at 30°C for 30 minutes and stopped by pipetting onto P81 paper. The unincorporated [γ -³³P]ATP is removed by washing and the incorporated radioactivity is measured using a radioactivity scintillation counter. Alternatively, the reaction is stopped by heating to 100°C in the presence of SDS loading buffer and visualized on a 12% SDS polyacrylamide gel by autoradiography. Incorporated radioactivity is corrected for reactions carried out in the absence of PKIN or in the presence of the

15 inactive kinase, K38A.

In yet another alternative, adenylate kinase or guanylate kinase activity may be measured by the incorporation of ³²P from gamma-labeled ³²P -ATP into ADP or GDP using a gamma radioisotope counter. The enzyme, in a kinase buffer, is incubated together with the appropriate nucleotide mono-phosphate substrate (AMP or GMP) and ³²P-labeled ATP as the phosphate donor. The

20 reaction is incubated at 37°C and terminated by addition of trichloroacetic acid. The acid extract is neutralized and subjected to gel electrophoresis to separate the mono-, di-, and triphosphonucleotide fractions. The diphosphonucleotide fraction is cut out and counted. The radioactivity recovered is proportional to the enzyme activity.

In yet another alternative, other assays for PKIN include scintillation proximity assays (SPA),

25 scintillation plate technology and filter binding assays: Useful substrates include recombinant proteins tagged with glutathione transferase, or synthetic peptide substrates tagged with biotin. Inhibitors of PKIN activity, such as small organic molecules, proteins or peptides, may be identified by such assays.

Kinase activity of PKIN may be determined by its ability to convert polyphosphate substrate (PolyP) to ATP in the presence of ADP. PKIN and Poly P are incubated at 37°C for 40 minutes and

30 then at 90°C for 2 minutes in a buffer containing 50 mM Tris-HCl, pH 7.4, 40 mM ammonium sulfate, 4 mM MgCl₂, and 5 µM ADP. The reaction mixture is diluted 1:100 in 100 mM Tris-HCl (pH 8.0), 4 mM EDTA, which is then diluted 1:1 in luciferase reaction mixture (ATP Bioluminescence Assay Kit CLS II; Boehringer Mannheim). The ATP generated is then quantitated using a luminometer

(Kornberg, A. et al. (1999) Annu. Rev. Biochem. 68:89-125; Ault-Riché, D. et al. (1998) J. Bacteriol. 180:1841-1847).

Kinase activity of PKIN, as measured by phosphorylation of substrate, may be determined using an immune complex kinase assay well known in the art. COS7 cells are transfected with an expression plasmid constructed from a FLAG tag expression vector (pME18S-FLAG) containing PKIN DNA. A control transfection using vector alone without the PKIN DNA insert is done in parallel. After 48 hours, the cells are lysed in buffer A (20 mM HEPES-NaOH, pH 7.5, 3 mM MgCl₂, 100 mM NaCl₂, 1 mM dithiothreitol, 1 mM phenylmethanesulfonyl fluoride, 1 µg/ml leupeptin, 1 mM EGTA, 1 mM Na₃VO₄, 10 mM NaF, 20 mM β-glycerophosphate, and 0.5% Triton X-100) and 10 centrifuged at 14,000 rpm. Supernatants are incubated with anti-FLAG antibody (M2 monoclonal antibody; Eastman Kodak Co.) in a 50% slurry of protein A-Sepharose (Amersham Pharmacia Biotech) for 1.5 hours at 4°C. Immune complexes are precipitated and washed twice in buffer A and twice in buffer B (20 mM HEPES-NaOH, pH 7.5, 1 mM dithiothreitol, 10 µM Na₃VO₄, 2 mM β-glycerophosphate, 0.1 mM phenylmethanesulfonyl fluoride, 0.1 µg/ml leupeptin, 0.1 mM EGTA.) 15 Precipitates are incubated in buffer B containing 0.17 mg/ml myelin basic protein (MBP) (Sigma), 20 µM ATP, and 5 µCi of [γ-³²P]ATP (NEN Life Science Products) at 30°C for 20 minutes. The reaction is stopped by the addition of 4X Laemmli sample buffer (50 mM Tris-HCl, pH 6.8, 2% SDS, 30 mM dithiothreitol, and 10% glycerol) and heated at 95°C for 5 minutes. Proteins are separated by SDS-polyacrylamide gel electrophoresis and radioactivity incorporated into MBP is detected by 20 autoradiography (Nakano, K. et al. (2000) J. Biol. Chem. 275:20533-20539.)

In yet another alternative, an assay for PanK activity of PKIN includes the enzyme preparation method as described in Vallari, D.S. et al., (1987) J. Biol. Chem. 262:2468-247. Pantothenate kinase-specific activities in cell lysates are calculated as a function of protein concentration with the assay being linear with respect to both time and protein input. Protein 25 concentrations are measured using the Bradford assay using bovine γ-globulin as a standard. Standard assays contain D-[1-¹⁴C]pantothenate (45.5 µM; specific activity 55 mCi/mmol), ATP (2.5 mM, pH 7.0), MgCl₂ (2.5 mM), Tris-HCl (0.1 M, pH 7.5), and 15µg of protein from a soluble cell extract in a total volume of 40 µl. The mixture is incubated for 10 min. at 37 °C, and the reaction is stopped by depositing a 30-µl aliquot onto a Whatman DE81 ion-exchange filter disc which is then 30 washed in three changes of 1% acetic acid in 95% ethanol (25 ml/disc) to remove unreacted pantothenate. 4'-Phosphopantothenate is quantitated by counting the dried disc in 3 ml of scintillation solution (Rock, supra).

XVIII. Enhancement/Inhibition of Protein Kinase Activity

Agonists or antagonists of PKIN activation or inhibition may be tested using assays described in section XVII. Agonists cause an increase in PKIN activity and antagonists cause a decrease in PKIN activity.

- 5 Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious
10 to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
7482896	1	7482896CD1	23	7482896CB1
7483046	2	7483046CD1	24	7483046CB1
71636374	3	71636374CD1	25	71636374CB1
7480597	4	7480597CD1	26	7480597CB1
3227248	5	3227248CD1	27	3227248CB1
4207273	6	4207273CD1	28	4207273CB1
7483334	7	7483334CD1	29	7483334CB1
7483337	8	7483337CD1	30	7483337CB1
6035509	9	6035509CD1	31	6035509CB1
7373485	10	7373485CD1	32	7373485CB1
5734965	11	5734965CD1	33	5734965CB1
7473788	12	7473788CD1	34	7473788CB1
3107989	13	3107989CD1	35	3107989CB1
7482887	14	7482887CD1	36	7482887CB1
2963414	15	2963414CD1	37	2963414CB1
7477139	16	7477139CD1	38	7477139CB1
55009053	17	55009053CD1	39	55009053CB1
7474648	18	7474648CD1	40	7474648CB1
7483053	19	7483053CD1	41	7483053CB1
7483117	20	7483117CD1	42	7483117CB1
7484498	21	7484498CD1	43	7484498CB1
7638121	22	7638121CD1	44	7638121CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank NO:	ID	Probability Score	GenBank Homolog
1	7482896CD1	g852055	2.90E-167	[Homo sapiens] casein kinase I-alpha Fish,K.J. et al., (1995) J. Biol. Chem. 270:14875-14883	
2	7483046CD1	g2736151	4.20E-167	[Rattus norvegicus] myotonic dystrophy kinase-related Leung,T. et al., (1998) Mol. Cell. Biol. 18:130-140	
3	71636374CD1	g7549223	0	[Mus musculus] PALS1 (proteins associated with Lin-7, a membrane-associated guanylate kinase)	
4	7480597CD1	g2224679	1.40E-97	[Homo sapiens] KIAA0369 doublecortin-like kinase Nagase,T. et al., (1997) DNA Res. 4:141-150	Kamborov,E. et al., (2000) J. Biol. Chem. 275:11425-11431
5	3227248CD1	g6690020	4.90E-199	[Mus musculus] pantothenate kinase 1 beta Rock,C.O. et al. (2000) J. Biol. Chem. 275:1377-1383	Burgess,H.A. et al. (1999) J. Neurosci. Res. 58:567-575
6	4207273CD1	g4028547	4.70E-68	[Dictyostelium discoideum] MEK kinase alpha Chung,C.Y. et al. (1998) Genes Dev. 12:3564-3578	
7	7483334CD1	g479173	1.70E-251	[Homo sapiens] protein kinase Schultz,S.J. et al. (1994) Cell Growth Differ. 5:625-635	
8	7483337CD1	g9280288	3.10E-27	[Arabidopsis thaliana] receptor protein kinase Kaneko,T. et al. (2000) DNA Res. 7:217-221	
9	6035509CD1	g6110362	3.60E-76	[Homo sapiens] Trα2 and NCK interacting kinase, splice variant 7 Fu,C.A. et al. (1999) J. Biol. Chem. 274:30729-30737	
10	7373485CD1	g4200446	0	[Mus musculus] FYVE finger-containing phosphoinositide kinase Shisheva,A. et al. (1999) Mol. Cell. Biol. 19:623-634	
11	5734965CD1	g2905643	4.60E-109	[Klebsiella pneumoniae] ribitol kinase Heuel,H. et al. (1998) Microbiology 144(Pt 6):1631-9	
12	7473788CD1	g7160989	1.70E-148	[Homo sapiens] serine/threonine protein kinase Ruiz-Perez,V.L. et al. (2000) Nat. Genet. 24(3):283-6	
13	3107989CD1	g6690020	1.60E-129	[Mus musculus] pantothenate kinase 1 beta Rock,C.O. et al. (2000) J. Biol. Chem. 275:1377-1383	

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank NO:	ID Score	Probability	GenBank Homolog
14	7482387CD1	g205662	3.90E-48	[Rattus norvegicus] nucleoside diphosphate kinase Kimura, N. et al. J. Biol. Chem. (1990) 265:15744-15749	
15	2963414CD1	g6524024	8.90E-106	[Mus musculus] mammalian inositol hexakisphosphate kinase 1 Sajardi, A. et al. Curr. Biol. (1999) 9: 1323-1326	
16	7477139CD1	g6472874	0	[Mus musculus] Nck-interacting kinase-like embryo specific kinase Nakano, K. et al. J. Biol. Chem. (2000) 275:20533-20539	
17	55009053CD1	g15131540	0	[Homo sapiens] (AJ316534) serine/threonine protein kinase [f1][Homo sapiens]	
18	7474648CD1	g14346040	0	[Homo sapiens] serine/threonine kinase PSKH2	
19	7483053CD1	g5419753	0	[Homo sapiens] RET tyrosine kinase receptor Bordeaux, M.C. et al. (2000) EMBO J. 19:4056-4063	
20	7483117CD1	g644770	2.70E-136	[Xenopus laevis] Wee1A kinase Mueller, P.R. et al. (1995) Mol. Biol. Cell 6:119-134	
21	7484498CD1	g3599509	0	[Mus musculus] rho/raf-interacting citron kinase Di Cunto, F. et al. (1998) J. Biol. Chem. 273:29706-29711	
22	7638121CD1	g212661	1.20E-60	[Gallus gallus] smooth muscle myosin light chain kinase precursor Olson, N.J. et al. (1990) Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288	

Table 3

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	7482896CD1	337	S105 S122 S199 S237 S242 S27 S49 S7 S96 T109 T146 T184 T228 T243 T323 T327 T38 Y209 Y274	N167 N215 N3	Eukaryotic protein kinase domain: Y17-F211 Protein kinases signatures and profile: T112-R168	HMMER-PFAM PROFILE-SCAN
2	7483046CD1	475		S161 S280 S307 S363 S407 S430 T455	PROTEIN KINASE DOMAIN DM00004 P35506 19-273: L19-Y274 P54367 22-276: L19-Y274 P48730 11-265: L19-Y274 B56406 19-273: L19-Y274 CASEIN KINASE I TRANSFERASE SERINE/THREONINE PROTEIN ATP-BINDING ISOFORM ALPHA CK1 ALPHA MULTIGENE PD006522: R282-G324 Tyrosine kinase catalytic domain PR00109: Y126-M144 Kinase Protein Domain PD00584: V20-G29 Protein kinases ATP-binding region signature: I23-K46 Serine/Threonine protein kinases active-site signature: F132-M144 signal_cleavage: M1-G40 Eukaryotic protein kinase domain: F71-F337	BLAST-PRODOM BLIMPS-PRINTS BLIMPS-PRODOM MOTIFS MOTIFS SPSCAN HMMER-PFAM

Table 3

SEQ ID NO.	Incyle Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					PROTEIN KINASE DOMAIN DM00004 Q09013 83-336; I73-R325 S42867 75-498; I73-H252 I38133 90-369; E72-L220 P53894 353-658; L74-G215	BLAST-DOMO
					KINASE PHORBOL ESTER BINDING DYSTROPHRY KINASE RELATED CDC42 BINDING SIMILAR SERINE/THREONINE PROTEIN GENGHIS KHAN PD0012280; L25-D70 Tyrosine kinase catalytic domain PR00109; M148-S161, S185-L203, C257-E279	BLAST-PRODOM
3	71636374CD1	675	S130 S14 S143 S25 S383 N82 S432 S517 S5562 S569 S576 S581 S646 S84 T137 T253 T270 T422 T465 T514 T558 T584 T97 Y593		GUANYLATE KINASE DM00755 A57653 370-570; P475-P670 P54936 769-955; R478-P670 I38757 709-898; Q474-P670 P310 61529-718; R480-P670	SPSCAN HMMER-PFAM BLAST-DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					PROTEIN DOMAIN SH3 KINASE GUANYLATE TRANSFERASE ATPBINDING REPEAT GMP MEMBRANE PD001338: T514-E620	BLAST-PRODOM
					SIMILAR TO GUANYLATE KINASE PD065809: G41-Q337	BLAST-PRODOM
					Guanylate kinase protein BL00856: V511-V531, D539-R586	BLIMPS-BLOCKS
					SH3 domain signature PR00452: D386-E395, I348-P358, L369-Q384	BLIMPS-PRINTS
					PDZ domain (Also known as DHR or GLGF). PDZ: I256-S335, SH3 domain SH3:I348-Q415	HMMER-PFAM
					ATP/GTP-binding site motif A (P-loop): A404-S411	HMMER-PFAM
					Guanylate_Kinase signature and profile: T514-V531	MOTIFS
4	7480597CD1	835	S11 S153 S174 S223 S249 S271 S292 S349 S369 S380 S389 S393 S405 S525 S54 S59 S633 S713 T129 T194 T246 T278 T300 T319 T33 T451 T477 T499 T514 T545 T610 T63 T681 T790 T808	N768	Eukaryotic protein kinase domain kinase: Y543-I800 Protein kinases signatures and profile: D640-I697	HMMER-PFAM
					PROTEIN KINASE DOMAIN DM00004 S57347 21-266: V548-T790 P08414 44-285: I549-T790 A44412 16-262: I549-A791 JU0270 16-262: I549-A791	PROFILE-SCAN BLAST-DOOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
5	3227248CD1	373	S100 S283 S285 S330 S47 T10 T167 T209 T226 T230 T244 T34	N103 N72	KINASE PROTEIN TRANSFERASE ATP-BINDING SERINE/THREONINE PROTEIN PHOSPHORYLATION RECEPTOR TYROSINE PROTEIN PRECURSOR TRANSMEMBRANE PD000001: E609-V693 Octicosapeptide repeat p PF00564: Y543-S397, H605-BLIMPS-M655, K473-G526 Tyrosine kinase catalytic domain PR00109: L618-I631, H654-V672 Protein kinases ATP-binding region signature: I549-K572 Serine/Threonine protein kinases active-site signature: I660-V672	BLAST-PRODOM-BLIMPS-PFAM
6	4207273CD1	735	S100 S111 S113 S124 S152 S170 S179 S185 S186 S20 S202 S215 S221 S225 S240 S267 S271 S302 S459 S503 S729 S9 T10 T105 T13 T30 T402 T417 T425 T469 T626 T663 T669 T84 Y512	N289 N312 N341 N392 N400 N61 N624 N647	PROTEIN KINASE DOMAIN DM000004 A48084 98-348:K470-A722 DM00004 Q01389 11 176-1430:K470-A722 DM00004 P41892 11-249:G471-R719 DM00004 Q10407 826-1084:K470-A722	BLAST-PRODOM
					KINASE PROTEIN TRANSFERASE ATP-BINDING SERINE/THREONINE PROTEIN PHOSPHORYLATION RECEPTOR TYROSINE PROTEIN PRECURSOR TRANSMEMBRANE PD000001:L631-P673, E472-C537, Y533-S633, S701-S734	BLAST-PRODOM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
7	7483334CD1	506	S148 S206 S243 S319 S325 S354 S47 T197 T288 T293 T308 T321 T373 T386 T402 T403 T479	N181 N345 N377 N401	Tyrosine kinase catalytic domain signature PR00109:M547-N560, Y583-L601, G636-I646, S655-M677 Eukaryotic protein kinase domain kinase:W468-L731 Protein_Kinase_Atp L474-K496 Protein_Kinase_St V589-L601 Protein kinases signatures and profile protein kinase_tyr_prf:Y569-A619 PROTEIN KINASE DOMAIN DM00004 P519546-248:L7-S247 P5195718-251:L7-S247 P5195510-261:V6-S247 Q08942(22-269:M9-S247)	BLIMPS-PRINTS HMMER-PFAM MOTIFS MOTIFS PROFILE-SCAN BLAST-DOMO
8	7483337CD1	2014	S1076 S1151 S1177 S1217 S1274 S1279 S1454 S15 S1515 S1679 S1700 S1811 S1833 S1887 S1890 S1999	N1024 N1119 N1338 N1599 N1674 N307 N371 N409	Tyrosine kinase catalytic domain signature PR00109:M779-K92, H117-L135, S183-N205, Y226-A248 Eukaryotic protein kinase domain kinase:Y4-V257 Protein_Kinase_Atp I10-K33 Protein_Kinase_St V123-L135 Protein kinases signatures and profile protein_kinase_tyr_prf:MI03-M156 PROTEIN KINASE DOMAIN DM00004 I38044 I00-349:I1295-P1549 I49663 I94-437:E1341-P1549 A53800 I119-368:R1343-P1549 S29851 I57-404:E1341-P1549	BLIMPS-PRINTS HMMER-PFAM MOTIFS MOTIFS PROFILE-SCAN BLAST-DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			S203 S25 S321 S337 S401 S531 S56 S565 S599 S81 S843 S863 S887 S900 T1091 T1099 T1113 T1187 T1189 T1234 T1401 T1543 T1605 T1634 T1660 T1872 T1895 T2010 T280 T494 T517 T524		Tyrosine kinase catalytic domain signature PR00109: Y1414-V1432, V1483-H1505, Q1529-A1551 transmembrane domain transmem_domain:P1367-N1387	BLIMPS-PRINTS HMMER
			T533 T537 T680 T687 T699 T702 T703 T753 T795 T811 T835 T909 Y1225 Y1997 Y907		Eukaryotic protein kinase domain pkinase:E1280-P1549 Protein kinases signatures and profile protein_kinase_tyr_pf1.L1400-E1457 Atp_Gtp_A_G672-S679	HMMER-PFAM PROFILE-SCAN MOTIFS
9	6035509CD1	348	S101 S171 S199 S271 S50 S7 T178 T213 T311 T318 T33	N177	PROTEIN KINASE DOMAIN DM00004 P10676 I18-272;I17-P270 A53714 I17-262;I17-S271 P38692 24-266;E19-S271 P08458 20-262;I21-S271	BLAST-DOMO
10	7373485CD1	2042	S1020 S105 S1079 S1125 S1130 S1148 S13	N1061 N1274 N1647 N1671	Tyrosine kinase catalytic domain signature PR00109:H134-L152, G181-I191, W250-V272 Eukaryotic protein kinase domain pkinase:W15-I281 Protein_Kinase_Atp_I21-K44 Protein_Kinase_St_I1140-L152 Protein kinases signatures and profile protein_kinase_tyr_pf1.M120-T172 Probable phosphatidyl inositol 4-phosphate 5-kinase FAB1 EC 2.7.1.68 1-phosphatidyl inositol 4-	BLIMPS-PRINTS HMMER-PFAM MOTIFS PROFILE-SCAN BLAST-PRODOM

Table 3

SEQ NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			S1377 S1419 S1429 S1440 S1466 S1483 S1488 S1544 S1545 S1620 S1639 S1648 S168 S1685 S1703 S1784 S1785 S1830 S1899 S228 S244 S257 S261 S286 S291 S367 S423 S475 S502 S576 S789 S810 S835 S85 S872 S896 S977 T1005 T1013 T109 T1149 T1295 T1386 T1524 T1567 T1670 T1674 T1681 T1708 T1722 T173 T1743 T1813 T1852 T1872 T1909 T1970 T341 T342 T591 T666 T731 T782 T976 T984 Y1290 Y1716Y1933 Y659	N1870 N303 N310 N333	phosphate 5-kinase diphosphoinositide transferase PD136025;H461-F821, W1147-K1437, L1375- S1702, K638-K767, P1663-V1780, D1372-Q1458, F959-11069, R960-D1053, F200-R262, D1895- S1950; PDD041996;L1974-W2035 5-KINASE PHOSPHATIDYL INOSITOL 4- PHOSPHATE KINASE TYPE TRANSFERASE DIPHOSPHOINOSITIDE 1-PHOSPHATIDYL INOSITOL 4-PHOSPHATE II ALPHA PHOSPHATIDYL INOSITOL PD002308;P1751- G1966, L1974-F2028, I493-H533 FYVE zinc finger FYV:Q153-C213 PIP5K Phosphatidylinositol-4-phosphate 5-Kinase PIPS:R1791-F2028	BLAST- PRODOM
11	5734965CD1	551	S107 S176 S21 S257 S368 S502 S54 T183 T286 T334 T356 T403 T66 Y526 Y531	N127 N219	FGGY family of carbohydrate kinases: L423-A490 FGGY FAMILY OF CARBOHYDRATE KINASES DM01757P21939 1-480; V13-A184 XYLULOKINASE DM02388 P181571-492; T383- E539	HMMER- PFAM BLAST- DOMO BLAST- DOMO

Table 3

SEQ ID NO:	Incye Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					FGGY FAMILY OF CARBOHYDRATE KINASES DM01757 P37677 L-479; R10-D260 FGGY FAMILY OF CARBOHYDRATE KINASES DM01757 P46834 L-488; Y11-V268 MPA43 PROTEIN PD130314;Y13-1210	BLAST- DOMO BLAST- DOMO BLAST- PRODOM PRODOM BLIMPS- BLOCKS
12	7473788CD1	485	S10 S159 S3 S343 S362 N405 S415 S417 T115 T192 T466 T469 T76 Y119		Eukaryotic protein kinase domain: F93-Q345 PROTEIN KINASE DOMAIN DM00004 P54644 122 362: I95-S342 PROTEIN KINASE DOMAIN DM00004 P28178 155 393: I95-L341 PROTEIN KINASE DOMAIN DM08046 P05986 L-397: K65-P372 P06244 L-396: F93-P372	HMMER- PFAM BLAST- DOMO BLAST- DOMO HMMER- PFAM BLAST- DOMO
13	3107989CD1	282	S148 S152 S192 S194 S239 S78 T118 T138 T1139 T153 T36	N12	signal_cleavage:M1-A24 signal_cleavage: M1-A27	SPSCAN SPSCAN

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
14	7482887CD1	151	S42 S97 T35 Y141		NUCLEOSIDE DIPHOSPHATE KINASES DM00773 P48817 3-152:17-Y150 DM00773 I39074 19-168:17-Y150 DM00773 P50590 1-150:17-Y150	BLAST- DOMO
15	2963414CD1	410	S134 S156 S276 S318 T259 T361 T374 T383 T62	N117 N290	NUCLEOSIDE DIPHOSPHATE NUCLEOSIDE TRANSFERASE NDK NDP ATP BINDING PROTEIN I PRECURSOR PD001018:17-Y150 Nucleoside diphosphate kinases proteins BL00469:E77-L131 Nucleoside diphosphate kinases NDK:17-A151 Nucleoside diphosphate kinases active site ndp_kinase:G96-R142	BLAST- PRODOM BLAST- PRODOM BLIMPS- BLOCKS HMMER- PFAM PROFILE- SCAN

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
16	7477139CD1	1581	S101 S1107 S1112 S1139 S1178 S1233 S1291 S1346 S136 S1400 S1426 S1435 S148 S1537 S1577 S211 S283 S376 S398 S580 S671 S676 S700 S709 S718 S749 S807 S84 S890 S891 S892 S910 T1071 T1123 T1194 T1367 T1508 T1546 T1556 T246 T276 T294 T357 T573 T664 T690 T899 T981 T992	N1137 N1201 N146 N654 N668 N990	PROTEIN KINASE DOMAIN DM00004 P1067 6 18-272;Y83-P302 DM00004 A537 14 17-262;L143-S304 DM00004 P38692 24-266;S84-C293, K29-N57 DM00004 P50527 388-627;K77-S304, I31-E65	BLAST_DO MO
17	55009053CD1	1084	S1024 S1031 S1038 S1042 S1058 S157 S172 S231 S25 S422 S452 S478 S52 S521 S552 S569 S604 S623 S709 S80 S862 S882 S895 S914 S962 S968 S969 S981 S988 T102 T1037 T167 T230 T256 T263 T37 T420 T48 T543 T593 T631 T8 Y1005	N953	Serine/Threonine protein kinases active-site signature I139-I151 Protein kinases signatures and profile protein_kinase_tyro.prft: L118-F173 Eukaryotic protein kinase domain pkinase: L15-F273	MOTIFS PROFILE-SCAN HMMER-PFAM BLIMPS-PRINTS
18	7474648CD1	600	S206 S331 S369 S425 S456 S543 S55 S571	N18 N495	Protein kinases ATP-binding region signature I284-K307	MOTIFS

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			S577 S585 T117 T14 T25 T299 T300 T356 T371 T395 T433 T58		Eukaryotic protein kinase domain pkinase: Y278-V535 Tyrosine kinase catalytic PR00109; M352-I365, Y388-BLIMPS-Y406, V458-E480	HMMER-PFAM
19	7483053CD1	1114	S1034 S104 S110 S131 S159 S173 S224 S363 S413 S457 S522 S561 S65 S670 S691 S696 S765 S811 S819 S836 S922 T1022 T1055 T1078 T261 T295 T315 T328 T350 T456 T492 T538 T564 T675 T729 T75 T847 T930 Y1096 Y483 Y905	N1092 N151 N199 N336 N343 N361 N367 N377 N394 N448 N468 N554 N834 N975 N98	PROTEIN KINASE DOMAIN DM00004 S57347[21-266; D279-L516 P08414 44-285; I280-S525 JN0323 25-268; I284-R523 S46284 28-274; I284-A526 signal peptide: M1-G28 Signal cleavage: M1-A26 Transmembrane domain: L13-F31 Protein kinases ATP-binding region signature L730-K758 Tyrosine protein kinases specific active-site signature L870-V882 Protein kinases signatures and profile protein_kinase_tyr.prf; D850-D903 Receptor_tyr_kin_ii.prf; R878-D925 Cadherin domain cadherin: P172-T261 Eukaryotic protein kinase domain pkinase: L724-L1005	BLIMPS-PRINTS BLAST-DOMO HMMER-PFAM SPSCAN HMMER HMMER-MOTIFS HMMER-MOTIFS HMMER-MOTIFS PROFILE-SCAN PROFILE-SCAN HMMER-PFAM HMMER-PFAM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Receptor tyrosine kinase BL00239; D903-Y952, P957-I1001, E775-V822, L851-R873, A876-E901 BL00240: K716-A764, A764-E818, D850-K887, E902-G949, G949-I1001 BL00790, G748-L801, A855-A876, A877-D903, Q910-W942, H968-L1016	BLIMPS-BLOCKS
20	7483117CD1	567	S162 S17 S206 S243 S278 S543 S552 S70 T112 T125 T22 T246 T344 T559 T68 Y238	N15 N332	Tyrosine kinase catalytic PR00109; V804-R817, Y864-V882, I913-L923, S932-C954, C976-F998 RECEPTOR KINASE PRECURSOR SIGNAL RET TYROSINE PROTOONCOGENE TYROSINE CRET TRANSFERASE PD014372: P273-K666, D360-V725; PD014143: Y30-C197; PD007958: V1010-G1063, PD010335; M1064-S1114	BLIMPS-PRINTS BLAST-PRODOM

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					WEE1 HOMOLOG WEE1LIKE PROTEIN KINASE MITOSIS TRANSFERASE TYROSINEPROTEIN ATPBINDING PHOSPHORYLATION PD028078: N483-G561	BLAST-PRODOM
21	7484498CD1	2054	S81 S93 S140 S248 S308 S361 S381 S386 S410 S436 S445 S480 S487 S501 S516 S529 S546 S577 S582 S699 S883 S888 S924 S1031 S1049 S1097 S1158 S1160 S1234 S1315 S1364 S1365 S1370 S1371 S1377 S1574 S1845 S1915 S1933 S2014 S2028 T83 T378 T498 T604 T840 T951 T956 T989 T1041 T1062 T1112 T1186 T1231 T1309 T1326 T1336 T1372 T1543 T1583	N1768	PROTEIN KINASE DOMAIN DM00004 P47817 211-470: L213-A477 P30291 300-559: E214- A477 P54350 241-507: E214-A477 A57247 104. 343: K217-1347, A366-R474	BLAST- DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			T1775 T1787 T1943 T1955 T1961 T2015 Y763		CITRON PROTEIN COILED COIL RHO/RACINTERACTING KINASE PD155701: F859-L1071 PD143273: G1439-V1631 PD082663: L1201-P1389 PD143272: A1881-V2054	BLAST- PRODOM
22	7638121CD1	1665	S97 S152 S156 S163 S242 S364 S450 S459 S491 S493 S528 S536 S588 S762 S827 S875 S915 S917 S929 S947 S961 S997 S1087 S1147	N1005	PROTEIN KINASE DOMAIN DM00004 Q09013183-336: V99-L349 S42867 75-498: S101-G241, I258-S445 S42864 41-325: E98-G241, N249-L349 P33894 353-658: L102-G241 I258-L349	BLAST- DOMO

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
			S1203 S1336 S1351 S1365 S1391 S1434 S1446 S1459 S1461 S1521 T59 T230 T257 T312 T668 T870 T966 T1211 T1310 T1320 T1638		Tyrosine kinase catalytic domain signature PR00109: S341-E363, L387-A409, L238-Y251, Y274-M292 KINASE PROTEIN TRANSFERASE ATPBINDING SERINE/THYROONINEPROTEIN PHOSPHORYLATION RECEPTOR TYROSINEPROTEIN PRECURSOR TRANSMEMBRANE PD000001: V256-V327, S323-D365, S380-P423 PROTEIN KINASE DOMAIN DM00004	BLIMPS- PRINTS BLAST- PRODOM

Table 4

Polynucleotide SEQ ID NO:	Incyte ID	Sequence Length	Selected Fragments	Sequence Fragments	5' Position	3' Position
23	7482896CB1	1014	982-1014	GNN g7899226_000043_0021 .edit	1	1014
24	7483046CB1	1530	719-770, 1-61, 1036-1104, 1271-1461, 313-464	71581296V1 71581650V1 71601507V1 55143579J1 71579961V1 55140831J1	889 778 1124 1 266 118	1476 1455 1530 272 884 522
25	71636374CB1	3150	1294-1806, 1-115, 2593-2616	183812R7 (CARDNOT01) 7676680H1 (NOSETUE01) 825204H1 (BRAHDIT10) 5223511F9 (OVARDIT07) GBI.g7452884_edit GBI.g8919852_edit 7214961H1 (LUNGFFEC01) 7710619J1 (TESTTUE02) 7391509H1 (LIVRFFEE02) 595804H1 (BRATNOT05)	2581 250 25 1225 1125 1099 1 1611 751 2796 2211	3148 864 804 1397 2085 1898 250 2273 1302 3150 2832
26	7480597CB1	2901	1907-1981, 1-156, 748-1606, 255-313	55150024J1 55073631J1 55150108J1 2841337T6 (DRGLNOT01) 55144761T1 5543295F7 (TESTNOC01) GNN g7658410_0000016_0021 56001404J1	1377 630 1711 2251 2132 137 1 1790	2056 1518 2070 2901 2833 574 2013 2434

Table 4

Polynucleotide SEQ ID NO:	Incyte ID	Sequence Length	Selected Fragments	Sequence Fragments	5' Position	3' Position
27	3227248CB1	1671	1-85,	70944845V1	997	1646
		1593-1671,	7207691H1 (FIBPFEA01)	451	1050	
		1327-1360	8283762T1 (LIVRNNON08)	180	562	
			GBl.g9796547_edit	1	1539	
			71281138V1	1089	1671	
			5260904F6 (CONDUTU01)	569	1065	
28	4207273CB1	2577	1-1641,	5543515F6 (TESTNOC01)	907	1376
		1845-1889	5357164H1 (TESTNOC01)	238	440	
			55144823H1	2112	2377	
			GNN.g9230839_000001_002	1	1293	
			55073166T1	1115	1773	
			4919885T6 (TESTNOT11)	1445	2141	
29	7483334CB1	2110	1-640,	71341632V1	1559	2110
		1255-1314,	71341335V1	1145	1708	
		948-1005	940589R6 (ADRENOT03)	1916	2110	
			6512850H1 (THYMDIT01)	1007	1688	
			6102073H1 (UTRENOT09)	797	1087	
			4970029F7 (KIDEUNC10)	1	677	
			7659406H1 (OVARNOE02)	509	1081	
30	7483337CB1	7093	1-3002,	7383958R8 (FTUBTUE01)	1	694
		4789-5840,	3245584H1 (BRAINOT19)	2681	2928	
		7069-7093,	72334852V1	5219	5761	
		3561-3671	7383958F8 (FTUBTUE01)	537	1196	
			58002303T1	6221	7093	
			70771904V1	58851	6475	
			GNN.g6693375_000016_002	986	3303	
			.edit			
			55046508H1	2906	3666	

Table 4

Polymerotide SEQ ID NO:	Incyte ID	Sequence Length	Selected Fragments	Sequence Fragments	5' Position	3' Position
				5514427J1	5514	6397
				5208289H1 (BRAFNOT02)	4900	5138
				7036825F6 (UTRSTM(R02)	3953	4647
				55046508J1	3448	4132
				70772942V1	5079	5680
				6436908H1 (LUNGNON07)	908	1407
				GNN_g6721428_000012_004 edit	3780	6267
31	6035509CB1	1800	152-333, 1-25, 1463-1800, 770-862	71927475V1 6035509F8 (PTTUNOT06) 55071284J1 72420180D1 55071288J1	1340 848 818 1	1800 1614 1098 729
32	7373485CB1	6347	4445-5413, 728-786, 6321-6347, 1497-3441, 4019-4079, 877-1082	72375809V1 8116978H1 (TONSDIC01) GNN_g6114949_010.edit5p 6919538R8 (PLACFER06) GNN_g6850654_000027_002 7368965H1 (ADREFEC01) 6460173H2 (OSTEUNC01) 6801172F6 (COLENOR03) 7212618T8 (LUNGFFEC01) 6919538F8 (PLACFER06) 55073317H1 580013367H1 7271932R8 (OVARDIJ01) 5623962R8 (THYMNOR02)	2075 1 480 1096 2075 1 659 1497 1156 998 1496 5742 5357 4290 3001 390 2592 4871 3712 1143 3387 5725 3542 4220 4544	2717 1096 2717 3728 1644 1496 6347 5883 4817 3001 390 2592 4871 3712 1143 3387 5725 4220 5050

Table 4

Polynucleotide SEQ ID NO:	Incyte ID	Sequence Length	Selected Fragments	Sequence Fragments	5' Position	3' Position
				72373545V1	1602	2203
				5623962F8 (THYMNOR02)	3970	4319
33	5734965CB1	1876	1-902	3254961T6 (OVARTUN01)	1276	1876
				5897065H1 (BRAVDIN03)	1	291
				70810516V1	181	806
				70162895V1	1002	1658
				70809778V1	915	1490
				70807962V1	302	989
34	7473788CB1	1487	1-121, 1450-1487	70995937V1 7177378H1 (BRAXDIC01) GNNNg3983331_000002_00 1 2.edit.1	1024 29 260	1487 554 1243
				70996158V1	594	1180
				7177363H2 (BRAXDIC01)	489	1507
35	3107989CB1	1884	1-306, 1253-1884	70942785V1 3107989F6 (BRSTTUT15)	1153 232	609
				7363877H1 (OVARDIC01) GNNNg9368012.edit1	1358 375	1884 1465
				2243306F6 (PANCUTTO2)	1	385
36	7482887CB1	1070	1-660, 891-948	56009164H1 GBI_g5815507.edit	1 612	725 997
				GBI_g9716284_order_0.edit2	988	1070
37	2963414CB1	2890	1-270, 1973-2064, 2658-2890, 726-1584	71882559V1 6741017F6 (BRAFEDIT02) 7252920V1 7090654H1 (BRAUTDR03)	470 1687 984 2284	1087 2299 1725 2876

Table 4

Polynucleotide SEQ ID NO:	Incyte ID	Sequence Length	Selected Fragments	Sequence Fragments	5' Position	3' Position
				7595015H1 (LIVRNOC07)	1	450
				71882107V1	424	985
				70523289V1	1123	1749
				7236335H1 (BRAINNOY02)	1904	2302
				2601908H1 (UTRSNOT10)	2660	2890
38	7477139CB1	5198	2528-2698, 1296-2145, 2792-4455, 528-724, 177-214	GNN g1149521_002 71143326V1 55117016H1 2879284F6 (UTRSTUT05) 3900926H1 (LUNGNON03) GNN g2780172_002.edit 72615067V1 6775332H1 (OVARDIR01) 7369332H1 (ADREFEC01)	948 4891 1 4388 3689 3433 701 4605 4063 1289	3957 5198 919 4874 3971 4943 1315 5193 4606 2065
39	55009053CB1	3969	1393-2860, 1-649	8036923H1 (SMCRUNE01) 72480126D1 7263320F6 (PROSTM02) 55009061H1 72476437D1 6583144F8 (BRAVTX01) 72508467V1 72509180V1 55009045J1	3325 1510 570 3306 1 2287 2494 288	3969 2343 1318 3968 452 3200 3329 982
40	7474648CB1	1803	198-1803	FL7474648_g7596812_0000 12_87981277_1_1 GNN g7596812_2	823 1 1	1497 1803 337
41	7483053CB1	3472	1-305, 3134-3472	GBl g69981824_000001.edit 2493520F6 (ADRETUT05)	1 2055	2525

Table 4

Polynucleotide SEQ ID NO:	Incyte ID	Sequence Length	Selected Fragments	Sequence Fragments	5' Position	3' Position	
				72498890V1	1524	2231	
				GNN g6981824_000001_042 edit	74	3187	
				55081239H1	847	1704	
				687245H1 (BRAGNON02)	2354	3059	
				7995993H1 (ADRETUC01)	2942	3472	
				7742567H1 (ADRETUE04)	647	1183	
42	7483117CB1	1704	1-342, 509-539, 582-58	GB1.g4153871_000001.edit 7369322F8 (ADREFEC01) GNN g4153871_006.edit	1536 343 1	1704 501 1678	
43	7484498CB1	6298	4050-4677, 1-195, 623-1785, 2406-2578, 3211-3637, 2139-2261	55058386H1 7073440H1 (BRAUTDR04) 7032228R8 (BRAXTDR12) 55053104J1 7014254F6 (KIDINNOC01) 7066607H1 (BRATNOR01)	601 5165 1618 4579 2926 55053152H1 55058386J1 7073642H1 (BRAUTDR04)	1357 5621 2321 5133 3470 848 1 5045 1564 1 701 5617 6892089F6 (BRAUTDR03) 8267244H1 (MIXDUNF04) 7076436H1 (BRAUTDR04) 7068147R8 (BRATNOR01) GNN g4508157_002.edit	5090 4401 3497 2294 4401 5097 4047 2708 1166 1941

Table 4

Polynucleotide SEQ ID NO:	Incyte ID	Sequence Length	Selected Fragments	Sequence Fragments	5' Position	3' Position
				7741468H1 (THYMNOE01)	3001	3627
				6850478H1 (BRAIFEN08)	5720	6298
				7068147F8 (BRATNOR01)	4092	4592
44	7638121CB1	5454	1718-3145, 1-989, 3982-4016	6756753J1 (SINTFER02) 7361161H1 (BRAIFEE05) 55057003J1 56000546J1 7354408H1 (HEARNON03)	3907 1 252 1303 5008	4637 637 937 2019 5454
				5863411F6 (MUSLTDT01) 71873215V1	3355 4520	4178 5227
				71873134V1	3114	3669
				6496171T6 (COLNNOT41)	4710	5416
				55141853J2	810	1390
				7647137H1 (UTRSTUE01)	1920	2257
				7600017R6 (ESOGTME01)	1475	2041
				6200811F6 (PITTUNON01)	3037	3632
				55052669H1	2245	3081

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID:	Representative Library
24	7483046CB1	COLCTUT03
25	71636374CB1	CARDNOT01
26	7480597CB1	DRGLNOT01
27	3227248CB1	COTRNOT01
28	4207273CB1	TESTNOC01
29	7483334CB1	ADRENOT03
30	7483337CB1	UTRSTM02
31	6035509CB1	PITUNOT06
32	7373485CB1	MCLDTXT02
33	5734965CB1	PROSTUS23
34	7473788CB1	BRAJNOT19
35	3107989CB1	STOMFET02
37	2963414CB1	SCORN0T04
38	7477139CB1	PLACFER06
39	55009053CB1	SINITME01
41	7483053CB1	BRAYDIN03
42	7483117CB1	ADREFEC01
43	7484498CB1	BRAITDR03
44	7638121CB1	MUSLTDR02

Table 6

Library	Vector	Library Description
ADREFEC01	pINCY	This large size-fractionated library was constructed using RNA isolated from adrenal tissue removed from a Caucasian female fetus who died from anencephalus after 16-weeks' gestation. Serology was negative. Family history included taking daily prenatal vitamins and mitral valve prolapse in the mother.
ADREN0T03	PSPORT1	Library was constructed using RNA isolated from the adrenal tissue of a 17-year-old Caucasian male, who died from cerebral anoxia.
BRAINOT19	pINCY	Library was constructed using RNA isolated from diseased brain tissue removed from the left frontal lobe of a 27-year-old Caucasian male during a brain lobectomy. Pathology indicated a focal deep white matter lesion, characterized by marked gliosis, calcifications, and hemosiderin-laden macrophages, consistent with a remote perinatal injury. This tissue also showed mild to moderate generalized gliosis, predominantly subpial and subcortical, consistent with chronic seizure disorder. The left temporal lobe, including the mesial temporal structures, showed focal, marked pyramidal cell loss and gliosis in hippocampal sector CA1, consistent with mesial temporal sclerosis. GFAP was positive for astrocytes. The patient presented with intractable epilepsy, focal epilepsy, hemiplegia, and an unspecified brain injury. Patient history included cerebral palsy, abnormality of gait, and depressive disorder. Family history included brain cancer.
BRAITDR03	PCDNA2.1	This random primed library was constructed using RNA isolated from allocortex, cingulate posterior tissue removed from a 55-year-old Caucasian female who died from cholangiocarcinoma. Pathology indicated mild meningeal fibrosis predominately over the convexities, scattered axonal spheroids in the white matter of the cingulate cortex and the thalamus, and a few scattered neurofibrillary tangles in the entorhinal cortex and the periaqueductal gray region. Pathology for the associated tumor tissue indicated well-differentiated cholangiocarcinoma of the liver with residual or relapsed tumor. Patient history included cholangiocarcinoma, post-operative Budd-Chiari syndrome, biliary ascites, hydrothorax, dehydration, malnutrition, oliguria and acute renal failure. Previous surgeries included cholecystectomy and resection of 85% of the liver.
BRAYDIN03	pINCY	This normalized library was constructed from 6.7 million independent clones from a brain tissue library. Starting RNA was made from RNA isolated from diseased hypothalamus tissue removed from a 57-year-old Caucasian male who died from a cerebrovascular accident. Patient history included Huntington's disease and emphysema. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48 -hours/round) reannealing hybridization was used. The library was linearized and recircularized to select for insert containing clones.
CARDNOT01	PBLUESCRIPT	Library was constructed using RNA isolated from the cardiac muscle of a 65-year-old Caucasian male, who died from a gunshot wound.

Table 6

Library	Vector	Library Description
COLCTUT03	pINCY	Library was constructed using RNA isolated from cecal tumor tissue removed from a 70-year-old Caucasian female during right hemicolectomy, open liver biopsy, flexible sigmoidoscopy, colonoscopy, and permanent colostomy. Pathology indicated invasive grade 2 adenocarcinoma forming an ulcerated mass 2 cm distal to the ileocecal valve and invading the muscularis propria. One regional lymph node (of 16) was positive for metastatic adenocarcinoma. Patient history included a deficiency anemia, malignant breast neoplasm, type II diabetes, hyperlipidemia, viral hepatitis, an unspecified thyroid disorder, osteoarthritis, a malignant skin neoplasm, and normal delivery. Family history included cardiovascular and cerebrovascular disease, hyperlipidemia, and breast and ovarian cancer.
COTRNOT01	pINCY	Library was constructed using RNA isolated from diseased transverse colon tissue obtained from a 26-year-old Caucasian male during a total abdominal colectomy and colostomy. Pathology indicated minimally active pancolitis with areas of focal severe colitis with perforation, consistent with Crohn's disease.
DRGLNOT01	pINCY	Library was constructed using RNA isolated from dorsal root ganglion tissue removed from the cervical spine of a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus, infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Surgeries included colonoscopy, large intestine biopsy, adenotonsillectomy, and nasopharyngeal endoscopy and biopsy; treatment included radiation therapy.
MCLDDT02	pINCY	Library was constructed using RNA isolated from treated umbilical cord blood dendritic cells removed from a male. The cells were treated with granulocyte/macrophage colony stimulating factor (GM-CSF), tumor necrosis factor alpha (TNF alpha), stem cell factor (SCF), phorbol myristate acetate (PMA), and ionomycin. The GM-CSF was added at time 0 at 100 ng/ml, the TNF alpha was added at time 0 at 2.5 ng/ml, the SCF was added at time 0 at 25 ng/ml. The PMA and ionomycin were added at 13 days for five hours. Incubation time was 13 days.
MUSLTDR02	PCDNA2.1	This random primed library was constructed using RNA isolated from right lower thigh muscle tissue removed from a 58-year-old Caucasian male during a wide resection of the right posterior thigh. Pathology indicated no residual tumor was identified in the right posterior thigh soft tissue. Changes were consistent with a previous biopsy site. On section through the soft tissue and muscle there was a smooth cystic cavity with hemorrhage around the margin on one side. The wall of the cyst was smooth and pale-tan. Pathology for the matched tumor tissue indicated a grade II liposarcoma. Patient history included liposarcoma (right thigh), and hypercholesterolemia. Previous surgeries included resection of right thigh mass. Family history included myocardial infarction and an unspecified rare blood disease.

Table 6

Library	Vector	Library Description
PITUNOT06	pINCY	Library was constructed using RNA isolated from pituitary gland tissue removed from a 55-year-old male who died from chronic obstructive pulmonary disease. Neuropathology indicated there were no gross abnormalities, other than mild ventricular enlargement. There was no apparent microscopic abnormality in any of the neocortical areas examined, except for a number of silver positive neurons with apical dendrite staining, particularly in the frontal lobe. The significance of this was undetermined. The only other microscopic abnormality was that there was prominent silver staining with some swollen axons in the CA3 region of the anterior and posterior hippocampus. Microscopic sections of the cerebellum revealed mild Bergmann's gliosis in the Purkinje cell layer. Patient history included schizophrenia.
PLACFER06	pINCY	This random primed library was constructed using RNA isolated from placental tissue removed from a Caucasian fetus who died after 16 weeks' gestation from fetal demise and hydrocephalus. Patient history included umbilical cord wrapped around the head (3 times) and the shoulders (1 time). Serology was positive for anti-CMV. Family history included multiple pregnancies and live births, and an abortion.
PROSTUS23	pINCY	This subtracted prostate tumor library was constructed using 10 million clones from a pooled prostate tumor library that was subjected to 2 rounds of subtractive hybridization with 10 million clones from a pooled prostate tissue library. The starting library for subtraction was constructed by pooling equal numbers of clones from 4 prostate tumor libraries using mRNA isolated from prostate tumor removed from Caucasian males at ages 58 (A), 61 (B), 66 (C), and 68 (D) during prostatectomy with lymph node excision. Pathology indicated adenocarcinoma in all donors. History included elevated PSA, induration and tobacco abuse in donor A; elevated PSA, induration, prostate hyperplasia, renal failure, osteoarthritis, renal artery stenosis, benign HTN, thrombocytopenia, hyperlipidemia, tobacco/alcohol abuse and hepatitis C (carrier) in donor B; elevated PSA, induration, and tobacco abuse in donor C; and elevated PSA, induration, hypercholesterolemia, and kidney calculus in donor D. The hybridization probe for subtraction was constructed by pooling equal numbers of cDNA clones from 3 prostate tissue libraries derived from prostate tissue, prostate epithelial cells, and fibroblasts from prostate tissue.
SCORN04	pINCY	Library was constructed using RNA isolated from cervical spinal cord tissue removed from a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus, infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Surgeries included colonoscopy, large intestine biopsy, adenotonsillectomy, and nasopharyngeal endoscopy and biopsy; treatment included radiation therapy.

Table 6

Library	Vector	Library Description
SINTME01	pINCY	This 5' biased random primed library was constructed using RNA isolated from ileum tissue removed from a 70-year-old Caucasian female during right hemicolectomy, open liver biopsy, flexible sigmoidoscopy, colonoscopy, and permanent colostomy. Pathology for the matched tumor tissue indicated invasive grade 2 adenocarcinoma forming an ulcerated mass, situated 2 cm distal to the ileocecal valve. Patient history included a malignant breast neoplasm, type II diabetes, hyperlipidemia, viral hepatitis, an unspecified thyroid disorder, osteoarthritis, a malignant skin neoplasm, deficiency anemia, and normal delivery. Family history included breast cancer, atherosclerotic coronary artery disease, benign hypertension, cerebrovascular disease, ovarian cancer, and hyperlipidemia.
STOMFET02	pINCY	Library was constructed using RNA isolated from stomach tissue removed from a Hispanic male fetus, who died at 18 weeks' gestation.
TESTNOC01	PBLUESCRIPT	This large size fractionated library was constructed using RNA isolated from testicular tissue removed from a pool of eleven, 10 to 61-year-old Caucasian males.
UTRSTM02	PCDNA2.1	This random primed library was constructed using pooled cDNA from two different donors. cDNA was generated using mRNA isolated from endometrial tissue removed from a 32-year-old female (donor A) and using mRNA isolated from myometrium removed from a 45-year-old female (donor B) during vaginal hysterectomy and bilateral salpingo-oophorectomy. In donor A, pathology indicated the endometrium was secretory phase. The cervix showed severe dysplasia (CIN III) focally involving the squamocolumnar junction at the 1, 6 and 7 o'clock positions. Mild koilocyotic dysplasia was also identified within the cervix. In donor B, pathology for the matched tumor tissue indicated multiple (23) subserosal, intramural, and submucosal leiomyomata. Patient history included stress incontinence, extrinsic asthma without status asthmaticus and normal delivery in donor B. Family history included cerebrovascular disease, depression, and atherosclerotic coronary artery disease in donor B.

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less; Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, ifasta, fastx, ifastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value= 1.06E-6; Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value= 1.0E-8 fastx score= 100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Atwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less

Table 7

Program	Description	Reference	Parameter Threshold
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) <i>Our World View, in a Nutshell</i> , Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value=1.0E-3 or less; Signal peptide hits: Score= 0 or greater
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score≥GCG-specified “HIGH” value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater

Table 7

Program	Description	Reference	Parameter Threshold
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Person, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Person, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22,
 - b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-22,
 - c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, and
 - d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.
2. An isolated polypeptide of claim 1 comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.
3. An isolated polynucleotide encoding a polypeptide of claim 1.
4. An isolated polynucleotide encoding a polypeptide of claim 2.
5. An isolated polynucleotide of claim 4 comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44.
6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
7. A cell transformed with a recombinant polynucleotide of claim 6.
8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
9. A method of producing a polypeptide of claim 1, the method comprising:
 - a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant

polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

- b) recovering the polypeptide so expressed.

5 10. A method of claim 9, wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

11. An isolated antibody which specifically binds to a polypeptide of claim 1.

10 12. An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44,
- b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:23-44,
- c) a polynucleotide complementary to a polynucleotide of a),
- d) a polynucleotide complementary to a polynucleotide of b), and
- e) an RNA equivalent of a)-d).

20 13. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 12.

14. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

- 25 a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

30 15. A method of claim 14, wherein the probe comprises at least 60 contiguous nucleotides.

16. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- 5 b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

17. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

10

18. A composition of claim 17, wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

19. A method for treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition of claim 17.

20. A method of screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- 20 a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

21. A composition comprising an agonist compound identified by a method of claim 20 and a pharmaceutically acceptable excipient.

25

22. A method for treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment a composition of claim 21.

30 23. A method of screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

24. A composition comprising an antagonist compound identified by a method of claim 23 and a pharmaceutically acceptable excipient.

25. A method for treating a disease or condition associated with overexpression of functional PKIN, comprising administering to a patient in need of such treatment a composition of claim 24.

26. A method of screening for a compound that specifically binds to the polypeptide of claim 1, the method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and
- 10 b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

27. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, the method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,
- b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and
- 20 c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

25
28. A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- 30 b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

29. A method of assessing toxicity of a test compound, the method comprising:
- a) treating a biological sample containing nucleic acids with the test compound,
 - b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 12 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 12 or fragment thereof,
 - c) quantifying the amount of hybridization complex, and
 - d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

- 10 30. A diagnostic test for a condition or disease associated with the expression of PKIN in a biological sample, the method comprising:
- a) combining the biological sample with an antibody of claim 11, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex, and
 - b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

- 15 20 25 31. The antibody of claim 11, wherein the antibody is:
- a) a chimeric antibody,
 - b) a single chain antibody,
 - c) a Fab fragment,
 - d) a F(ab')₂ fragment, or
 - e) a humanized antibody.

- 30 32. A composition comprising an antibody of claim 11 and an acceptable excipient.
33. A method of diagnosing a condition or disease associated with the expression of PKIN in a subject, comprising administering to said subject an effective amount of the composition of claim 32.

34. A composition of claim 32, wherein the antibody is labeled.

35. A method of diagnosing a condition or disease associated with the expression of PKIN in a subject, comprising administering to said subject an effective amount of the composition of claim 34.

5

36. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 11, the method comprising:

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, or an immunogenic fragment thereof, under conditions to elicit an antibody response,
- b) isolating antibodies from said animal, and
- c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

10

37. A polyclonal antibody produced by a method of claim 36.

38. A composition comprising the polyclonal antibody of claim 37 and a suitable carrier.

20 39. A method of making a monoclonal antibody with the specificity of the antibody of claim 11, the method comprising:

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22, or an immunogenic fragment thereof, under conditions to elicit an antibody response,
- b) isolating antibody producing cells from the animal,
- c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells,
- d) culturing the hybridoma cells, and
- e) isolating from the culture monoclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

25

30

40. A monoclonal antibody produced by a method of claim 39.

41. A composition comprising the monoclonal antibody of claim 40 and a suitable carrier.

42. The antibody of claim 11, wherein the antibody is produced by screening a Fab expression library.

5

43. The antibody of claim 11, wherein the antibody is produced by screening a recombinant immunoglobulin library.

44. A method of detecting a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22 in a sample, the method comprising:

- a) incubating the antibody of claim 11 with a sample under conditions to allow specific binding of the antibody and the polypeptide, and
- b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22 in the sample.

45. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22 from a sample, the method comprising:

- a) incubating the antibody of claim 11 with a sample under conditions to allow specific binding of the antibody and the polypeptide, and
- b) separating the antibody from the sample and obtaining the purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-22.

46. A microarray wherein at least one element of the microarray is a polynucleotide of claim 25 13.

47. A method of generating a transcript image of a sample which contains polynucleotides, the method comprising:

- a) labeling the polynucleotides of the sample,
- b) contacting the elements of the microarray of claim 46 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
- c) quantifying the expression of the polynucleotides in the sample.

48. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, and wherein said target polynucleotide is a polynucleotide of claim 12.

5

49. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

50. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is 10 completely complementary to at least 60 contiguous nucleotides of said target polynucleotide.

51. An array of claim 48, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to said target polynucleotide.

15 52. An array of claim 48, which is a microarray.

53. An array of claim 48, further comprising said target polynucleotide hybridized to a nucleotide molecule comprising said first oligonucleotide or polynucleotide sequence.

20 54. An array of claim 48, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

25 55. An array of claim 48, wherein each distinct physical location on the substrate contains multiple nucleotide molecules, and the multiple nucleotide molecules at any single distinct physical location have the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another distinct physical location on the substrate.

30 56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.
60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.
- 5 61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.
62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.
63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.
- 10 64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.
65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.
- 15 66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.
67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.
68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.
- 20 69. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.
70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.
- 25 71. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.
72. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.
73. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.
- 30 74. A polypeptide of claim 1; comprising the amino acid sequence of SEQ ID NO:19.
75. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.

76. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.
77. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.
- 5 78. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:23.
79. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:24.
80. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:25.
- 10 81. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:26.
82. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:27.
- 15 83. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:28.
84. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:29.
85. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:30.
- 20 86. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:31.
87. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:32.
- 25 88. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:33.
89. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:34.
90. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:35.
- 30 91. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:36.
92. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:37.

93. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:38.

94. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:39.

5 95. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:40.

96. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:41.

97. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:42.

10

98. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:43.

99. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:44.

<110> INCYTE GENOMICS, INC.
GURURAJAN, Rajagopal
BAUGHN, Mariah R.
WALIA, Narinder K.
ELLIOTT, Vicki S.
XU, Yuming
ARVIZU, Chandra
YAO, Monique G.
RAMKUMAR, Jayalaxmi
DING, Li
TANG, Y. Tom
HAFALIA, April J.A.
NGUYEN, Dannie B.
GANDHI, Ameena R.
LU, Yan
YUE, Henry
BURFORD, Neil
BANDMAN, Olga
TRIBOULEY, Catherine
LAL, Preeti G.
RECIPON, Shirley A.
LU, Dyung Aina M.
BOROWSKY, Mark L.
THORNTON, Michael
SWARNAKER Anita
THANGAVELU, Kavitha
KHAN, Farrah A.
ISON, Craig H.

<120> HUMAN KINASES

<130> PI-0262 PCT

<140> To Be Assigned

<141> Herewith

<150> 60/242,410; 60/244,068; 60/245,708; 60/247,672; 60/249,565;

60/252,730; 60/250,807

<151> 2000-10-20; 2000-10-27; 2000-11-03; 2000-11-09; 2000-11-16
2000-11-22; 2000-12-01

<160> 44

<170> PERL Program

<210> 1

<211> 337

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7482896CD1

<400> 1

Met Thr Asn Asn Ser Gly Ser Lys Ala Glu Leu Val Val Gly Gly

1

5

10

15

Ser Ser Pro Ala Pro Pro Glu Gly Pro Ser His Pro Arg Glu Pro
 1970 1975 1980
 Ser Thr Pro His Arg Tyr Arg Glu Gly Arg Thr Glu Leu Arg Arg
 1985 1990 1995
 Asp Lys Ser Pro Gly Arg Pro Leu Glu Arg Glu Lys Ser Pro Gly
 2000 2005 2010
 Arg Met Leu Ser Thr Arg Arg Glu Arg Ser Pro Gly Arg Leu Phe
 2015 2020 2025
 Glu Asp Ser Ser Arg Gly Arg Leu Pro Ala Gly Ala Val Arg Thr
 2030 2035 2040
 Pro Leu Ser Gln Val Asn Lys Val Trp Asp Gln Ser Ser Val
 2045 2050

<210> 22
 <211> 1665
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7638121CD1

<400> 22
 Met Gly Cys Cys Arg Leu Gly Cys Gly Ser Val Ala His
 1 5 10 15
 Ser Val Ser Gln Gly Leu Thr Asn His Pro Ser Met Val Gly Cys
 20 25 30
 Gly Trp His Pro Gly Leu Cys Gly Trp Gly Gly Leu His Ser
 35 40 45
 Ser Leu Pro Ala Leu Pro Gly Pro Pro Ser Met Gln Val Thr Ile
 50 55 60
 Glu Asp Val Gln Ala Gln Thr Gly Gly Thr Ala Gln Phe Glu Ala
 65 70 75
 Ile Ile Glu Gly Asp Pro Gln Pro Ser Val Thr Trp Tyr Lys Asp
 80 85 90
 Ser Val Gln Leu Val Asp Ser Thr Arg Leu Ser Gln Gln Glu
 95 100 105
 Gly Thr Thr Tyr Ser Leu Val Leu Arg His Met Ala Ser Lys Asp
 110 115 120
 Ala Gly Val Tyr Thr Cys Leu Ala Gln Asn Thr Gly Gly Gln Val
 125 130 135
 Leu Cys Lys Ala Glu Leu Leu Val Leu Gly Gly Asp Asn Glu Pro
 140 145 150
 Asp Ser Glu Lys Gln Ser His Arg Arg Lys Leu His Ser Phe Tyr
 155 160 165
 Glu Val Lys Glu Glu Ile Gly Arg Gly Val Phe Gly Phe Val Lys
 170 175 180
 Arg Val Gln His Lys Gly Asn Lys Ile Leu Cys Ala Ala Lys Phe
 185 190 195
 Ile Pro Leu Arg Ser Arg Thr Arg Ala Gln Ala Tyr Arg Glu Arg
 200 205 210
 Asp Ile Leu Ala Ala Leu Ser His Pro Leu Val Thr Gly Leu Leu
 215 220 225
 Asp Gln Phe Glu Thr Arg Lys Thr Leu Ile Leu Ile Leu Glu Leu
 230 235 240
 Cys Ser Ser Glu Glu Leu Leu Asp Arg Leu Tyr Arg Lys Gly Val

245	250	255
Val Thr Glu Ala Glu Val Lys Val Tyr Ile Gln Gln Leu Val Glu		
260	265	270
Gly Leu His Tyr Leu His Ser His Gly Val Leu His Leu Asp Ile		
275	280	285
Lys Pro Ser Asn Ile Leu Met Val His Pro Ala Arg Glu Asp Ile		
290	295	300
Lys Ile Cys Asp Phe Gly Phe Ala Gln Asn Ile Thr Pro Ala Glu		
305	310	315
Leu Gln Phe Ser Gln Tyr Gly Ser Pro Glu Phe Val Ser Pro Glu		
320	325	330
Ile Ile Gln Gln Asn Pro Val Ser Glu Ala Ser Asp Ile Trp Ala		
335	340	345
Met Gly Val Ile Ser Tyr Leu Ser Leu Thr Cys Ser Ser Pro Phe		
350	355	360
Ala Gly Glu Ser Asp Arg Ala Thr Leu Leu Asn Val Leu Glu Gly		
365	370	375
Arg Val Ser Trp Ser Ser Pro Met Ala Ala His Leu Ser Glu Asp		
380	385	390
Ala Lys Asp Phe Ile Lys Ala Thr Leu Gln Arg Ala Pro Gln Ala		
395	400	405
Arg Pro Ser Ala Ala Gln Cys Leu Ser His Pro Trp Phe Leu Lys		
410	415	420
Ser Met Pro Ala Glu Glu Ala His Phe Ile Asn Thr Lys Gln Leu		
425	430	435
Lys Phe Leu Leu Ala Arg Ser Arg Trp Gln Arg Ser Leu Met Ser		
440	445	450
Tyr Lys Ser Ile Leu Val Met Arg Ser Ile Pro Glu Leu Leu Arg		
455	460	465
Gly Pro Pro Asp Ser Pro Ser Leu Gly Val Ala Arg His Leu Cys		
470	475	480
Arg Asp Thr Gly Gly Ser Ser Ser Ser Ser Ser Ser Asp Asn		
485	490	495
Glu Leu Ala Pro Phe Ala Arg Ala Lys Ser Leu Pro Pro Ser Pro		
500	505	510
Val Thr His Ser Pro Leu Leu His Pro Arg Gly Phe Leu Arg Pro		
515	520	525
Ser Ala Ser Leu Pro Glu Glu Ala Glu Ala Ser Glu Arg Ser Thr		
530	535	540
Glu Ala Pro Ala Pro Pro Ala Ser Pro Glu Gly Ala Gly Pro Pro		
545	550	555
Ala Ala Gln Gly Cys Val Pro Arg His Ser Val Ile Arg Ser Leu		
560	565	570
Phe Tyr His Gln Ala Gly Glu Ser Pro Glu His Gly Ala Leu Ala		
575	580	585
Pro Gly Ser Arg Arg His Pro Ala Arg Arg Arg His Leu Leu Lys		
590	595	600
Gly Gly Tyr Ile Ala Gly Ala Leu Pro Gly Leu Arg Glu Pro Leu		
605	610	615
Met Glu His Arg Val Leu Glu Glu Ala Ala Arg Glu Glu Gln		
620	625	630
Ala Thr Leu Leu Ala Lys Ala Pro Ser Phe Glu Thr Ala Leu Arg		
635	640	645
Leu Pro Ala Ser Gly Thr His Leu Ala Pro Gly His Ser His Ser		
650	655	660
Leu Glu His Asp Ser Pro Ser Thr Pro Arg Pro Ser Ser Glu Ala		

665	670	675
Cys Gly Glu Ala Gln Arg Leu Pro Ser Ala Pro Ser Gly Gly Ala		
680	685	690
Pro Ile Arg Asp Met Gly His Pro Gln Gly Ser Lys Gln Leu Pro		
695	700	705
Ser Thr Gly Gly His Pro Gly Thr Ala Gln Pro Glu Arg Pro Ser		
710	715	720
Pro Asp Ser Pro Trp Gly Gln Pro Ala Pro Phe Cys His Pro Lys		
725	730	735
Gln Gly Ser Ala Pro Gln Glu Gly Cys Ser Pro His Pro Ala Val		
740	745	750
Ala Pro Cys Pro Pro Gly Ser Phe Pro Pro Gly Ser Cys Lys Glu		
755	760	765
Ala Pro Leu Val Pro Ser Ser Pro Phe Leu Gly Gln Pro Gln Ala		
770	775	780
Pro Leu Ala Pro Ala Lys Ala Ser Pro Pro Leu Asp Ser Lys Met		
785	790	795
Gly Pro Gly Asp Ile Ser Leu Pro Gly Arg Pro Lys Pro Gly Pro		
800	805	810
Cys Ser Ser Pro Gly Ser Ala Ser Gln Ala Ser Ser Ser Gln Val		
815	820	825
Ser Ser Leu Arg Val Gly Ser Ser Gln Val Gly Thr Glu Pro Gly		
830	835	840
Pro Ser Leu Asp Ala Glu Gly Trp Thr Gln Glu Ala Glu Asp Leu		
845	850	855
Ser Asp Ser Thr Pro Thr Leu Gln Arg Pro Gln Glu Gln Val Thr		
860	865	870
Met Arg Lys Phe Ser Leu Gly Gly Arg Gly Tyr Ala Gly Val		
875	880	885
Ala Gly Tyr Gly Thr Phe Ala Phe Gly Gly Asp Ala Gly Gly Met		
890	895	900
Leu Gly Gln Gly Pro Met Trp Ala Arg Ile Ala Trp Ala Val Ser		
905	910	915
Gln Ser Glu Glu Glu Gln Glu Ala Arg Ala Glu Ser Gln		
920	925	930
Ser Glu Glu Gln Glu Ala Arg Ala Glu Ser Pro Leu Pro Gln		
935	940	945
Val Ser Ala Arg Pro Val Pro Glu Val Gly Arg Ala Pro Thr Arg		
950	955	960
Ser Ser Pro Glu Pro Thr Pro Trp Glu Asp Ile Gly Gln Val Ser		
965	970	975
Leu Val Gln Ile Arg Asp Leu Ser Gly Asp Ala Glu Ala Ala Asp		
980	985	990
Thr Ile Ser Leu Asp Ile Ser Glu Val Asp Pro Ala Tyr Leu Asn		
995	1000	1005
Leu Ser Asp Leu Tyr Asp Ile Lys Tyr Leu Pro Phe Glu Phe Met		
1010	1015	1020
Ile Phe Arg Lys Val Pro Lys Ser Ala Gln Pro Glu Pro Pro Ser		
1025	1030	1035
Pro Met Ala Glu Glu Glu Leu Ala Glu Phe Pro Glu Pro Thr Trp		
1040	1045	1050
Pro Trp Pro Gly Glu Leu Gly Pro His Ala Gly Leu Glu Ile Thr		
1055	1060	1065
Glu Glu Ser Glu Asp Val Asp Ala Leu Leu Ala Glu Ala Ala Val		
1070	1075	1080
Gly Arg Lys Arg Lys Trp Ser Ser Pro Ser Arg Ser Leu Phe His		

1085	1090	1095
Phe Pro Gly Arg His Leu Pro Leu Asp Glu Pro Ala Glu Leu Gly		
1100	1105	1110
Leu Arg Glu Arg Val Lys Ala Ser Val Glu His Ile Ser Arg Ile		
1115	1120	1125
Leu Lys Gly Arg Pro Glu Gly Leu Glu Lys Glu Gly Pro Pro Arg		
1130	1135	1140
Lys Lys Pro Gly Leu Ala Ser Phe Arg Leu Ser Gly Leu Lys Ser		
1145	1150	1155
Trp Asp Arg Ala Pro Thr Phe Leu Arg Glu Leu Ser Asp Glu Thr		
1160	1165	1170
Val Val Leu Gly Gln Ser Val Thr Leu Ala Cys Gln Val Ser Ala		
1175	1180	1185
Gln Pro Ala Ala Gln Ala Thr Trp Ser Lys Asp Gly Ala Pro Leu		
1190	1195	1200
Glu Ser Ser Ser Arg Val Leu Ile Ser Ala Thr Leu Lys Asn Phe		
1205	1210	1215
Gln Leu Leu Thr Ile Leu Val Val Ala Glu Asp Leu Gly Val		
1220	1225	1230
Tyr Thr Cys Ser Val Ser Asn Ala Leu Gly Thr Val Thr Thr Thr		
1235	1240	1245
Gly Val Leu Arg Lys Ala Glu Arg Pro Ser Ser Pro Cys Pro		
1250	1255	1260
Asp Ile Gly Glu Val Tyr Ala Asp Gly Val Leu Leu Val Trp Lys		
1265	1270	1275
Pro Val Glu Ser Tyr Gly Pro Val Thr Tyr Ile Val Gln Cys Ser		
1280	1285	1290
Leu Glu Gly Ser Trp Thr Thr Leu Ala Ser Asp Ile Phe Asp		
1295	1300	1305
Cys Cys Tyr Leu Thr Ser Lys Leu Ser Arg Gly Gly Thr Tyr Thr		
1310	1315	1320
Phe Arg Thr Ala Cys Val Ser Lys Ala Gly Met Gly Pro Tyr Ser		
1325	1330	1335
Ser Pro Ser Glu Gln Val Leu Leu Gly Gly Pro Ser His Leu Ala		
1340	1345	1350
Ser Glu Glu Ser Gln Gly Arg Ser Ala Gln Pro Leu Pro Ser		
1355	1360	1365
Thr Lys Thr Phe Ala Phe Gln Thr Gln Ile Gln Arg Gly Arg Phe		
1370	1375	1380
Ser Val Val Arg Gln Cys Trp Glu Lys Ala Ser Gly Arg Ala Leu		
1385	1390	1395
Ala Ala Lys Ile Ile Pro Tyr His Pro Lys Asp Lys Thr Ala Val		
1400	1405	1410
Leu Arg Glu Tyr Glu Ala Leu Lys Gly Leu Arg His Pro His Leu		
1415	1420	1425
Ala Gln Leu His Ala Ala Tyr Leu Ser Pro Arg His Leu Val Leu		
1430	1435	1440
Ile Leu Glu Leu Cys Ser Gly Pro Glu Leu Leu Pro Cys Leu Ala		
1445	1450	1455
Glu Arg Ala Ser Tyr Ser Glu Ser Glu Val Lys Asp Tyr Leu Trp		
1460	1465	1470
Gln Met Leu Ser Ala Thr Gln Tyr Leu His Asn Gln His Ile Leu		
1475	1480	1485
His Leu Asp Leu Arg Ser Glu Asn Met Ile Ile Thr Glu Tyr Asn		
1490	1495	1500
Leu Leu Lys Val Val Asp Leu Gly Asn Ala Gln Ser Leu Ser Gln		

1505	1510	1515
Glu Lys Val Leu Pro Ser Asp Lys Phe Lys Asp Tyr Leu Glu Thr		
1520	1525	1530
Met Ala Pro Glu Leu Leu Glu Gly Gln Gly Ala Val Pro Gln Thr		
1535	1540	1545
Asp Ile Trp Ala Ile Gly Val Thr Ala Phe Ile Met Leu Ser Ala		
1550	1555	1560
Glu Tyr Pro Val Ser Ser Glu Gly Ala Arg Asp Leu Gln Arg Gly		
1565	1570	1575
Leu Arg Lys Gly Leu Val Arg Leu Ser Arg Cys Tyr Ala Gly Leu		
1580	1585	1590
Ser Gly Gly Ala Val Ala Phe Leu Arg Ser Thr Leu Cys Ala Gln		
1595	1600	1605
Pro Trp Gly Arg Pro Cys Ala Ser Ser Cys Leu Gln Cys Pro Trp		
1610	1615	1620
Leu Thr Glu Glu Gly Pro Ala Cys Ser Arg Pro Ala Pro Val Thr		
1625	1630	1635
Phe Pro Thr Ala Arg Leu Arg Val Phe Val Arg Asn Arg Glu Lys		
1640	1645	1650
Arg Arg Ala Leu Leu Tyr Lys Arg His Asn Leu Ala Gln Val Arg		
1655	1660	1665

<210> 23
<211> 1014
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7482896CB1

<400> 23
atgacaaaaca acagcggctc caaagccgaa ctgcgttgg gaggaaata ccaaactggtg 60
cggaagatcg ggtctggctc ctttggagac gtttatctgg gcatcacacc caccaacggc 120
gaggacgtag cagtgaagct ggaatctcg aagtcgaaac acccccagg tctgtatgg 180
agcaaaactct acacgattct tcaagggtggg gttggcatcc cccacatgca ctggatgg 240
cagaaaaaag acaacaatgt gctagtcatg gaccttctgg gaccggcct cgaagacctc 300
tttaatttct gttcaagaag gttcaccatg aaaactgtac ttatgttagc cgaccagatg 360
atcagcagaa ttgaatacgt gcatacaaag aattttctac accgagacat taaaccagat 420
aacttcctga tgggtactgg gcgtcactgt aataagttgt tccttattga ttttggttt 480
gccaaaaagt acagagacaa caggaccagg caacacatac cgtacagaga agataaacac 540
ctcattggca ctgtccgata tgccagcatc aatgcacatc ttggatttga gcagagccgc 600
cgagatgaca tggaaatcctt aggctacgtt ttcatgtatt ttaatagaac cagcctgccc 660
tggcaaggac taagggctat gacaaaaaaaaa caaaaatatg aaaagattag tgagaagaag 720
atgtccaccc ctgttgaagt tttatgtaa gggtttctg cagaattcgc catgtacttg 780
aactactgtc gtgggctgcg ctttgaggaa gtcccagatt acatgtatct gaggcagcta 840
ttccgcattc ttttcaggac cctgaaccac caatatgact acacatttga ttggacgatg 900
ttaaagcaga aagcagcaca gcaggcagcc tcttccagtg ggcagggtca gcaggccccaa 960
acccagacag gcaagcaaac tgaaaaaaaaa aagaataatg tgaaagataa ctaa 1014

<210> 24
<211> 1530
<212> DNA
<213> Homo sapiens

ccccaccgct accgcgaggg gcggacccgag ctgcgcaggg acaagtctcc tggccgcccc 6060
 ctggagcgag agaagtcccc cggcccgatg ctcaagcacgc ggagagagcg gtccccggg 6120
 aggctgtttg aagacagcag cagggggccgg ctgcctgcgg gagccgttag gaccccgctg 6180
 tcccaggta acaaggctctg ggaccagtct tcagtataaa tctcagccag aaaaaccaac 6240
 tcctcatctt gatctgcagg aaaacaccaa acacactatg gaactctgct gatgggaa 6298

<210> 44
 <211> 5454
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7638121CB1

<400> 44
 cacgcacacc gcacgtacgg gttgggccc agctgggta taagcgtat cccatgccc 60
 cctggccagg ctggggggca tttgcacatc tgcaaaggcc tcccagctg tcccagccct 120
 gccccagcct gggaccccca cattctactc accgtgtctc ctcagagggg ccagaaccct 180
 ccactgggaa gaggcaagtg gcggttaact tgggttccat aggaccctgt ccctgagagc 240
 gacagctgag ttatgtgatcc ctactgccc caccaactcc ttctgatcac ctggccagct 300
 gaggtcagag tgggagagggc agtggttcca ttgaaggagt actcctaact gtcagaagcc 360
 tggccgtca gatgggggt ctgtcgctt ggctgcggg ggtgttcaat tgcccacagt 420
 gtatctcagg gtctcaccaa ccataccaaatc atggtaggt gtggctggca cccagggtt 480
 tgtgctggg gaggtggctt ccacaggcc tccctgccc tcccaggccc cccatccatg 540
 caggtAACCA tcgaggatgt gcaggcacag acaggcgaa cggcccaatt cgaggctatc 600
 attgagggcg accccacagcc ctgggtgacc tggtaacaagg acagcttcca gctggggac 660
 agcacccggc ttatggcga gcaagaaggc accacatact ccctggtgc gaggcatatg 720
 gcctcgaagg atgcccggcgt ttacacctgc ctggcccaaa acactggtgg ccaggtgtc 780
 tgcaaggcag agctgttgtt gctgggggg gacaatgagc cggactcaga gaagcaaagc 840
 caccggagga agctgcactc ttctatgag gtcaaggagg agattggaa gggcgtgtt 900
 ggcttcgtaa aaagagtgcg gacacaaggaa aacaagatct tgcgtctgc caagttcatac 960
 cccctacggg gacaaactcg ggcccaggca tacaggagc gagacatctt ggccgcgtg 1020
 agccacccgc tggtcacggg gctgtggac cagtttgaga cccgcaagac cctcatcctc 1080
 atcctggagc tgcgtctatc cgaggagctg ctggaccggc tgcgttggaa gggcgtgtt 1140
 acggaggccg aggtcaagggt ctacatccag cagctggtgg aggggctgca ctacctgcac 1200
 agccatggcg ttctccacct ggacataaaag ccctctaaca tccctgatggt gcatctgccc 1260
 cggaaagaca taaaatctg cgtttggc tttggccaga acatcaccccc agcagagctg 1320
 cagttcagcc agtacggctc ccctgagttc gtctccccc agatcatcca gcaaaaccct 1380
 gtgagcgaag cttccgacat ttggccatg ggtgtcatct cctacctcag cctgacactgc 1440
 tcatccccat ttgcccggca gatgtaccgt gcccacccctcc tgaacgtctt ggagggcgc 1500
 gtgtcatggc gacggcccat ggctgcacccac ctcaagcggc acgccaaaga cttcatcaag 1560
 gctacgtgc agagagccccc tcaggcccg cctagtgcgg cccagtgctt ctcccaaaaa 1620
 tggttccatgaa aatccatgcc tgcggaggag gcccacttca tcaacaccaa gcaagctcaag 1680
 ttccctctgg cccgaagtcg ctggcagctg tccctgatga gctacaagtc catcctgggt 1740
 atgcgttcca tccctgatgt gctgcggggc ccacccgaca gcccctccctt cggcgttagcc 1800
 cggcacctct gcaaggacac tggggctcc tccatgttccct cctccctctt tgacaacagag 1860
 ctgcggccat ttgccccggc taatgttactg ccacccctcc cggtgacaca ctcacccactg 1920
 ctgcacccccc ggggcttccct gggcccttcg gcccacccctcc tgcggggccgt 1980
 gagcgttcca cccggggccccc agctccggctt gcatctcccg aggggtggccgg gcccacccggc 2040
 gcccgggtt gctgtggccctt gcaacggccatc tgggttccatcc ccaaggccgtt 2100
 gagagccctg agcacggggc cctggccccc gggagcggc ggcacccggc cggcggccgg 2160
 cacctgttca gggggccggta cattgcgggg ggcgttccag gctgtggccg gcaactgtatg 2220
 gagcaccggcg tgctggagga ggaggccccc agggaggagc agggccacccctt cctggccaaa 2280
 gccccctcat tgcgttccatcc cctccggctt gctgccttc gcaacccactt gggccctggc 2340
 cacagccactt ccctggaaaca tgcgttccatcc agcacccccc gccccctcttc ggaggccgtt 2400

ggtgaggcac agcgactgcc ttcagcccc tccggggggg cccctatca gacatgggg 2460
 caccctcagg gtc当地 aacttccatcc actgggtggcc acccaggcac tgctcagcca 2520
 gagaggccat ccccgacag cccttgggg cagccagccc ctttctgc当地 ccccaagcag 2580
 gttctgecc cccaggaggg ctgcagcccc cacccagcac ttgccccatg ccctcctggc 2640
 tcctccctc caggatctt caaagaggcc cccttagtac cctcaagccc cttctggga 2700
 cagccccagg cacccttgc ccctgc当地 gcaagcccc cattggactc taagatgggg 2760
 cctggagaca tctcttcc tgggagggca aaacccggcc cctgc当地 cccagggta 2820
 gcctcccagg cgagcttcc ccaagtgc当地 tccctcaggg tgggctcc caggtgggc 2880
 acagagctg gcccctccct ggtatggag ggctggaccc aggaggctga ggatctgtcc 2940
 gactccacac ccaccttgc当地 gcccctcag gaacaggctga cc当地 gcaaa gttctccctg 3000
 ggtgtcgcg ggggtacgc aggctggct ggctatggca ccttgc当地 tgggtggagat 3060
 gcagggggca tgctggggca gggcccatg tggccagga tagcctggc tgggtcccag 3120
 tcggaggagg aggagcagg ggaggccagg gctgagtc当地 agtc当地 gagga gcagcaggag 3180
 gccagggctg agagccact gcccaggc当地 agtgc当地 gagc ctgtgc当地 ggtcgccagg 3240
 gctccacca ggagcttcc agagccacc cc当地 gggagg acatgggca ggtctccctg 3300
 gtgcagatcc gggacctg local aggtgtgc当地 gagggcccg acacaatata cctggacatt 3360
 tccgaggtgg accccc当地 cctcaaccc tcaagactgt acgatataa gtacctccca 3420
 ttcgagttt当地 tgatcttgc当地 gaaagtcccc aagtc当地 gtc当地 agccagagcc gccc当地 3480
 atggctgagg aggagctggc cgagttcccg gagccacgt gggccctggc aggtgaactg 3540
 gggccccc当地 caggcctgg当地 gatcacagag gagtc当地 gagggatggc当地 gctgtggca 3600
 gaggctccg tgggaggaa ggc当地 aactggccgt tc当地 cggc当地 cacttc 3660
 cctgggaggc acctggccgt ggacgaggct gc当地 gagctgg ggctgc当地 gaggtgaag 3720
 gcctccgtgg agc当地 acatcc cccgatcc tggcaggc当地 aaggcaggc cggaggctt ggagaaggag 3780
 gggccccc当地 ggaaggaccc aggccctgtc tccctccggc tctcaggctt gagagactgg 3840
 gaccgaggc当地 cgacattcc aagggaggctc tcaagatgaga ctgtggctt gggccaggta 3900
 gtgc当地 actgg cctgcccagg gtc当地 agccctggc aggccacctg gagcaaagac 3960
 ggagccccc当地 tggagagcag cagccgtglocal ctcatctgt cc当地 accctcaa gaacttccag 4020
 ct当地 ctgacca tccctgggtt ggtggctgag gacccctgg tgc当地 acactg cagcgtgagc 4080
 aatgc当地 ctgg gacactgtac caccacggc当地 gtccctccgg aaggcaggacg cccctcatct 4140
 tc当地 gcatgaccc cggatatacg ggagggttac ggc当地 atgggggg tgc当地 ctgtgtt ctggagccc 4200
 gtggaaatcc acggccctgt gacctacatt gtgc当地 agtca gctt当地 agaggcc 4260
 accacactgg cctccgacat ct当地 tggactgc tgc当地 tacactgca cc当地 agcaact ctccccc当地 4320
 ggc当地 acctaca ccttccgac当地 ggc当地 atgtgtc agcaaggc当地 gaatgggtcc ctacaggc 4380
 ccctccgaggc aagtccctt gggaggccc agccacctgg cctctgaggc ggagagccag 4440
 gggccgttag cccaaaccctt gcccaggcaca aagacactgg cattccagac acagatccag 4500
 agggccgct tcaaggctggt gggcaatgc tggagaagg cc当地 agggccggc当地 ggc当地 ctggcc 4560
 gccaagatca tcccttacca ccccaaggac aagacaggc当地 tgctgc当地 gaatcaggcc 4620
 ct当地 aaggggcc tgc当地 ccaccctggc cagtc当地 gagc cagccctactt cagccccc当地 4680
 cacctggtgc tcaatcttggc gctgtgtt ctggccaggc tgctccctg cctggccagg 4740
 agggccctt actc当地 agtca acgggttag gactactgt ggc当地 agatgtt gagtggccacc 4800
 cagtc当地 actgc当地 acaaccaggca catccctgac ctggacactgca ggtccaggaa catgatc当地 4860
 accgaataaca acctgtctaa ggtcggtgac ctggc当地 atg cagaggcct cagccaggag 4920
 aagggtgtc cctc当地 gagacaa gttcaaggac tacctagaga cc当地 atggctcc agagcttcc 4980
 gagggccagg gggctgttcc acagacagac atctgggca tgggtgtgac agc当地 ctatc 5040
 atgctgagcg cccaggatacc ggtgaggc当地 gaggggtgac ggc当地 acctgca gagaggactg 5100
 cgcaaggggc tggtccggct gagccgtgc tacggggcc tgc当地 cgggggg cggc当地 ctggcc 5160
 ttccctgac当地 gcaactctgtg cggccaggccc tggggccggc cctgc当地 gagctgc当地 5220
 cagtgccctg ggctaaacaga ggaggccc当地 gctt当地 cggccggc当地 cgtacccctt 5280
 cctaccggc当地 ggctgc当地 cgtc当地 aatgc当地 gagacgc当地 gctgctgtac 5340
 aagaggcaca acctggccca ggtgc当地 gggc当地 cccacacc ttggtccccc 5400
 cgctgggggt cgctgc当地 gagac ggc当地 caataa aacgc当地 acag cc当地 ggccgaga aaaa 5454

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
25 April 2002 (25.04.2002)

PCT

(10) International Publication Number
WO 02/033099 A3

(51) International Patent Classification²: C12N 15/54,
9/12, C12Q 1/68, 1/48, A01K 67/027, C07K 16/40, G01N
33/50, A61K 38/45

(21) International Application Number: PCT/US01/47728

(22) International Filing Date: 20 October 2001 (20.10.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/242,410 20 October 2000 (20.10.2000) US
60/244,068 27 October 2000 (27.10.2000) US
60/245,708 3 November 2000 (03.11.2000) US
60/247,672 9 November 2000 (09.11.2000) US
60/249,565 16 November 2000 (16.11.2000) US
60/252,730 22 November 2000 (22.11.2000) US
60/250,807 1 December 2000 (01.12.2000) US

(71) Applicant (for all designated States except US): INCYTE GENOMICS, INC. [US/US]; 3160 Porter Drive, Palo Alto, CA 94304 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): GURURAJAN, Rajagopal [US/US]; 5591 Dent Avenue, San Jose, CA 95118 (US). BAUGHN, Mariah, R. [US/US]; 14244 Santiago Road, San Leandro, CA 94577 (US). CHAWLA, Narinder, K. [US/US]; 33 Union Square, #712, Union City, CA 94587 (US). ELLIOTT, Vicki, S. [US/US]; 3770 Polton Place Way, San Jose, CA 95121 (US). XU, Yuming [US/US]; 1739 Walnut Drive, Mountain View, CA 94040 (US). ARVIZU, Chandra [US/US]; 490 Sherwood Way #1, Menlo Park, CA 94025 (US). YAO, Monique, G. [US/US]; 1189 Woodgate Drive, Carmel, IN 46033 (US). RAMKUMAR, Jaya [IN/US]; 34359 Maybird Circle, Fremont, CA 94555 (US). DING, Li [CN/US]; 3353 Alma Street #146, Palo Alto, CA 94306 (US). TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). HAFALIA, April, J., A. [US/US]; 2227 Calle de Primavera, Santa Clara, CA 95054 (US). NGUYEN, Dannie, B. [US/US]; 1403 Ridgewood Drive, San Jose, CA 95118 (US). GANDHI, Ameena, R. [US/US]; 705 5th Avenue, San Francisco, CA 94118 (US). LU, Yan [CN/US]; 3885 Corrina Way, Palo Alto, CA 94303 (US). YUE, Henry [US/US]; 826 Lois Avenue, Sunnyvale, CA 94087 (US). BURFORD, Neil [GB/US]; 105 Wildwood Circle,

Durham, CT 06422 (US). BANDMAN, Olga [US/US]; 366 Anna Avenue, Mountain View, CA 94043 (US). TRIBBLE, Catherine, M. [FR/US]; 1121 Tennessee, #5, San Francisco, CA 94107 (US). LAL, Preeti, G. [IN/US]; P.O. Box 5142, Santa Clara, CA 95056 (US). RECIPON, Shirley, A. [US/US]; 85 Fortuna Avenue, San Francisco, CA 94115 (US). LU, Dzung, Aina, M. [US/US]; 233 Coy Drive, San Jose, CA 95123 (US). BOROWSKY, Mark, L. [US/US]; 122 Orchard Avenue, Redwood City, CA 94061 (US). THORNTON, Michael [US/US]; 9 Medway Road, Woodside, CA 94062 (US). SWARNAKER, Anita [CA/US]; 8 Locksley Avenue, #5D, San Francisco, CA 94122 (US). THANGAVELU, Kavitha [IN/US]; 1950 Montecito Avenue #23, Mountain View, CA 94304 (US). KHAN, Farrah, A. [IN/US]; 3617 Central Road, #102, Glenview, IL 60025 (US). ISON, Craig, H. [US/US]; 1242 Weathersfield Way, San Jose, CA 95118 (US).

(74) Agents: HAMLET-COX, Diana et al.; Incyte Genomics, Inc., 3174 Porter Drive, Palo Alto, CA 94304 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:
9 October 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN KINASES

(57) Abstract: The invention provides human human kinases (PKIN) and polynucleotides which identify and encode PKIN. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of PKIN.

WO 02/033099 A3

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/47728

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/54	C12N9/12	C1201/68	C1201/48	A01K67/027
C07K16/40	G01N33/50	A61K38/45		

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12Q A01K C07K G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, MEDLINE, SEQUENCE SEARCH, WPI Data, PAJ, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	<p>WO 01 38503 A (PLOWMAN GREGORY D ; CLARY DOUGLAS (US); SUGEN INC (US); WHYTE DAVID) 31 May 2001 (2001-05-31)</p> <p>* Sequence "SGK003_ID#NA_22" has 100% identity in a 1014nt overlap to SEQ ID NO.23. Sequence "SGK003_ID#AA_79" has 100% identity to SEQ ID NO.1 over a 337aa overlap *</p> <p>page 125; figures 1,2</p> <p>* Sequence "SGK058_ID#AA_106" has 100% identity over a 278aa overlap to SEQ ID NO.6. Sequence "SGK058_ID#NA_49" has 100% identity in a 834nt overlap to SEQ ID NO.28 *</p> <p>page 135</p> <p>page 146</p> <p>page 232</p> <p>page 250</p> <p>page 273</p>	<p>1-20, 23, 26-56, 61, 78, 83</p>

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
8 July 2003	04.08.03

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl. Fax: (+31-70) 340-3016	Meacock, S

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/47728

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	page 291, line 14 -page 292, line 8 page 306, line 15 - line 28 WO 01 98342 A (GLAXO GROUP LTD ;MURDOCK PAUL R (GB); SMITHKLINE BEECHAM PLC (GB);) 27 December 2001 (2001-12-27) SEQ ID NO.10 shows 100% identity over 1014nt overlap to SEQ ID NO.23 of the present application. SEQ ID NO.32 shows 100% identity over 337aa overlap with SEQ ID NO.1 * page 25 -page 26 page 29 page 47 -page 50	1-20,23, 26-56,78
X	FISH KIMBERLY J ET AL: "Isolation and Characterization of Human Casein Kinase I-epsilon (CKI), a Novel Member of the CKI Gene Family." JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 25, 1995, pages 14875-14883, XP002177865 ISSN: 0021-9258 cited in the application page 14877, left-hand column; figures 1,2	1-20,23, 26-56,78
X	WO 94 17189 A (SALK INST FOR BIOLOGICAL STUDI) 4 August 1994 (1994-08-04) * SEQ ID NO.11 shows 91% identity in a 1014nt overlap to SEQ ID NO.23 of the present application. SEQ ID NO.23 shows 91% identity over 335aa overlap to SEQ ID NO.1 * page 83 -page 87	1-20,23, 26-56,78
X	ROWLES J ET AL: "PURIFICATION OF CASEIN KINASE I AND ISOLATION OF CDNAS ENCODING MULTIPLE CASEIN KINASE I-LIKE ENZYMES" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 88, no. 21, 1991, pages 9548-9552, XP001119756 ISSN: 0027-8424	1,3,12
Y	* Figure 2 sequence shows 91% identity to SEQ ID NO.1 over 324aa overlap, and SEQ ID NO.23 over 971nt overlap * abstract; figure 2	13-20, 23, 26-56,78
	-/-	

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/47728

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PULGAR VICTOR ET AL: "The recombinant alpha isoform of protein kinase CK1 from Xenopus laevis can phosphorylate tyrosine in synthetic substrates." EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 242, no. 3, 1996, pages 519-528, XP001119751. ISSN: 0014-2956	1,3,12
Y	* Figure 1 sequence shows 91% identity to SEQ ID NO.1 over 335aa overlap * abstract; figure 1	13-20, 23, 26-56,78
X	GREEN C L ET AL: "Identification of four alternatively spliced isoforms of chicken casein kinase I alpha that are all expressed in diverse cell types" GENE, ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, NL, vol. 216, no. 1, August 1998 (1998-08), pages 189-195, XP004149296 ISSN: 0378-1119	1,3,12
Y	abstract; figure 1 * CKIalphaS sequence shows 91% identity to SEQ ID NO.1 over 335aa overlap * page 193, right-hand column	13-20, 23, 26-56,78
P,X	DATABASE EMBL 'Online' 1 March 2001 (2001-03-01) "Hypothetical protein FLJ23074" Database accession no. Q9H5T2 XP002246601 * 99.4% identity over 168aa overlap to SEQ ID NO.6 * the whole document	1-20,23, 26-55, 61,83
E	WO 02 14355 A (MERCK PATENT GMBH ;SCHARM BURKHARD (DE)) 21 February 2002 (2002-02-21) * SEQ ID NO.1 has 99.8% identity over 1137nt overlap to SEQ ID NO.28 of the present application; SEQ ID NO.4 has 100% identity over 233aa to SEQ ID NO.6 of the present application * abstract; claim 2 page 1 -page 3	1-20,23, 26-55, 61,83
		-/-

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/47728

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>GRAVES D J: "Powerful tools for genetic analysis come of age" TRENDS IN BIOTECHNOLOGY, ELSEVIER, AMSTERDAM, NL, vol. 17, no. 3, March 1999 (1999-03), pages 127-134, XP004157733 ISSN: 0167-7799 page 127, right-hand column page 130, left-hand column page 131, right-hand column page 132, left-hand column, paragraph 2</p>	46-55
A	<p>CHUNG CHANG Y ET AL: "A novel, putative MEK kinase controls developmental timing and spatial patterning in Dictyostelium and is regulated by ubiquitin-mediated protein degradation." GENES & DEVELOPMENT, vol. 12, no. 22, 15 November 1998 (1998-11-15), pages 3564-3578, XP002246600 ISSN: 0890-9369 * MEC kinase alpha has 47% identity over 247aa overlap to SEQ ID NO.6 * abstract; figure 1</p>	1-20, 23, 26-55, 61, 83

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/47728

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. Claims Nos.: 21, 22, 24 and 25
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

Inventions 1 and 6 (corresponding to SEQ ID NOS. 1, 6, 23 and 28): Claims 1-55 (all partially) and Claims 56, 61, 78 and 83 (all completely)
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claim 19 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Although claims 33 and 35 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.2

Claims Nos.: 21, 22, 24 and 25

Present Claims 21, 22, 24 and 25 relate to a compound defined by reference to a desirable characteristic or property, namely ant/agonist activity to the polypeptide of Claim 1.

The cited claims cover all compounds having this characteristic or property, whereas the application provides no support within the meaning of Art. 6 PCT and/or disclosure within the meaning of Art. 5 PCT for such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible.

Independent of the above reasoning, the claims also lack clarity (Art. 6 PCT). An attempt is made to define the product by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims 1-55 (all partially),
56 and 78 (both completely)

An isolated polypeptide which comprises the amino acid sequence of SEQ ID NO.1, comprises a polypeptide comprising a naturally-occurring amino acid sequence at least 90% identical to said polypeptide, or is a biologically active or immunogenic fragment of the amino acid sequence of SEQ ID NO.1; a method of producing, purifying or detecting said polypeptide; an isolated antibody which specifically binds said polypeptide; compositions comprising, and methods of making, said antibody; an isolated polynucleotide encoding said polypeptide or fragment; a recombinant polynucleotide comprising a promoter sequence operably linked to said polynucleotide; a cell transformed with, or a transgenic organism comprising, said recombinant polynucleotide; an isolated polynucleotide comprising a naturally occurring sequence at least 90% identical to SEQ ID NO.23; a polynucleotide complementary to said isolated polynucleotide or an RNA equivalent thereof; an isolated polynucleotide comprising at least 60 contiguous nucleotides of said polynucleotide; an array comprising said polynucleotide; methods of assessing toxicity of a test compound using said polynucleotide; a method of screening a compound for effectiveness in altering expression of said polynucleotide; a method of diagnosing a condition or disease using said polynucleotide or antibody; a method of generating a transcript image of a sample; a method of screening a compound for effectiveness as an agonist or antagonist of, or which specifically binds to, or that modulates the activity of, said polypeptide; a composition comprising an agonist or antagonist identified by said screening method and a method of treating a disease using said agonist or antagonist.

Inventions 2-22: Claims 1-55 (all partially),
Claims 57-77 and 79-99 (all completely)

Idem as for invention 1, but relating to an isolated polypeptide comprising the amino acid sequence of SEQ ID NOs.2-22 with the corresponding nucleotide sequences of SEQ ID NOs.24-44, respectively. Hence, invention 2 relates to SEQ ID NOs.2 and 24, invention 3 relates to SEQ ID NOs.3 and 25, and so on, with invention 22 relating to SEQ ID NOs.22 and 44.

In the interests of conciseness, the subject matter (which includes the associated aspects of encoding polynucleotides, antibodies, methods etc) of the inventions has been defined

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

explicitly only for the first invention, and the additional inventions defined only by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/47728

Patent document cited in search report	Publication date		Patent family member(s)	Publication date
WO 0138503	A 31-05-2001	AU CA EP JP WO	1926001 A 2394803 A1 1240194 A2 2003514583 T 0138503 A2	04-06-2001 31-05-2001 18-09-2002 22-04-2003 31-05-2001
WO 0198342	A 27-12-2001	AU BR CA CZ EP NO WO	6867101 A 0111877 A 2414005 A1 20024148 A3 1292617 A1 20026162 A 0198342 A1	02-01-2002 24-06-2003 27-12-2001 14-05-2003 19-03-2003 21-02-2003 27-12-2001
WO 9417189	A 04-08-1994	CA EP JP WO US US US US	2132452 A1 0632832 A1 7505057 T 9417189 A2 6060296 A 5627064 A 5756289 A 5686412 A	04-08-1994 11-01-1995 08-06-1995 04-08-1994 09-05-2000 06-05-1997 26-05-1998 11-11-1997
WO 0214355	A 21-02-2002	AU WO EP	9174501 A 0214355 A2 1307566 A2	25-02-2002 21-02-2002 07-05-2003